

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 3, 2005, 12:34:58 ; Search time 367.375 Seconds
(without alignments)
4093.201 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

US-08-625-101-1
; Sequence 1, Application US/08625101
; Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3768 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..3765
 US-08-625-101-1

Alignment Scores:

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RESULT 2
US-08-356-786-1
; Sequence 1, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3768
OTHER INFORMATION: /note= "product = "cerB-b2"
S-08-356-786-1

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  Percent Local Similarity: 73.23%
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  Matches: 919
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Db 2461 GACCTGTAACCTGGTGTATGCAGATTGCCAAGGGGATGAGTACCTGGAGGATGTGCGG 2520
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Db 2521 CTGTAACAGGAGNCTTGGCGGCTCGGAACGTGCTGTCAAGAGTCCCAACCATGTCAAA 2580
QY 653 ----- 653
Db 2581 ATTACAGACTTTCGGGCTGGCTCGGCTGCTGACATTGACGAGACAGAGTACCATGCAGAT 2640
QY 653 ----- 653

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QY 653 ----- 653
Db 2701 CACCAGAGTATGTGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
QY 653 ----- 653
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QY 653 ----- 653
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QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProIleu 664
Db 2941 AGGAGCCCCCAGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGGCCCGCAGCTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCAGTCTGGAGAGCATGATGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTATCCCGCAGCGGCTTCTTCTGTCCAGACCTGCCCGCGCGCTGGG 3120
QY 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCATGCTCCACCACAGGACCGCAGCTCATCTACCAGGAGTGGCGTGGGACCTGCACA 3180
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGGAGCCCTCTGAAGAGAGGGCCCCCAGGTCTCCACTGGCACCTCCGAAGGG 3240
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGTTGACCTGGGAATGGGGCAGCCAGGGGCTGCAAGC 3300
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProIleu 784
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QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
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QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCCAGCATGTTTCGGCCCCCAGCCCCCTTCGCCCGAGAGGGCCCTCTGCTGCTGCC 3480
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGGTGCCACTCTGGAAGGCCCAAGACTCTCTCCCGAGGAAAGATGGGGTC 3540
QY 845 ValIleAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
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QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCCCTCAGCCCCCACCCTCTCTGCTTCCAGCCAGGCTTCGACACCTC 3660
QY 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGAGCCAGGACCCACAGAGCGGGGGCTCCACCCAGCACCTTTCAAAGGACA 3720
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAACCCAGAGTACCTGGGGTCTGGAGCTGCCAGTG 3765

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RESULT 3
US-09-048-804-1
; Sequence 1, Application US/09048804
; Patent No. 5968748
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
; TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,804
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4473 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; ANTI-SENSE: No
; US-09-048-804-1

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservatives: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 2 Gaps: 1

US-09-493-480-6 (1-919) x US-09-048-804-1 (1-4473)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLeuLeuArgLeuProAlaSerProGlu 40
Db 235 GCGAGCACCAAGTGTGACCGCGCACAGACATGAAGCTCGGGCTCCCTGCCAGTCCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCCACTGGACATGCTCCGCCACCTCTACAGGGCTGCGAGGTGGTGGAGGAAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACTCACCTACCTGCGCCCAATGCGAGCTGTCTCTCTGCGAGGATATCCAGGAGGTG 414
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTAGCTGCTATCCCTCACACCAAGTGGAGGAGGTCCCTGCGAGGCTGCGG 474
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120

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Db 535 GACCCGCTGAAACAATACCACTCCCTGTCAAGGGGCTCCCAAGAGGCTGCGGGAGCTG 594
QY 141 GlnLeuArgSerLeuThrGluIleLeuGlyGlyValLeuLeuIleGlnArgAsnProGln 160
Db 595 CAGCTTCGAAGCCTCACAGAGATCTTGAAAGAGGGGTCTTGATCCAGCGGAACCCCAAG 654
QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 655 CTCCTCTACCAAGCACACGATTTTGTGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 714
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 775 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGGATTGTCAAGGCTGACGGCCTGCTGTCTGT 834
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
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QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 895 GCTGCGGGCTGCACGGGGCCCAAGCACTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
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QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 1375 GAGACTCTGGAAGAGATCACAGTTTACATATATACATCTCAGCATGTCGCGACAGCTGCT 1434
QY 421 AspLeuSerValPheGlnAsnLeuValIleArgGlyArgIleLeuHisGlnGlyAla 440
Db 1435 GACCTCAGCGCTTCCGAACCTGCAAGTAATCCGGGAGCGAATTTCTGCACAAATGGCGCC 1494
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1495 TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGCTGGGGCTGGCTGCTGCTGCTGCTGCTGCT 1554
QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480

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Db 1615 CCCTGGGACCAAGCTCTTTCCGAACCCGACCAAGCTCTGCTCCACACTGCGCAACCGGCCA 1674
Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1675 GAGGACAGAGTGTGGGCGAGGGCTGCTGCCACAGCTGTGCCCGCGAGGCGCACTGC 1734
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1735 TGGGGTCCAGGGCCACCCAGTGTGTCACTGACGACAGTTCCTTGGGGCCAGGAGTGC 1794
Qy 541 ValGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
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Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
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Qy 665 AspSerThrPheTyrArgSerLeuLeuAspAspMetGlyAspLeuValAspAla 684
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Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
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Qy 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
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QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
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RESULT 5

US-09-663-834A-3
; Sequence 3, Application US/09663834A
; Patent No. 6613567
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
; FILE REFERENCE: RTS-0033
; CURRENT APPLICATION NUMBER: US/09/663,834A
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)... (3942)
US-09-663-834A-3

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-663-834A-3 (1-4473)

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Db 235 GCGAGCACCAAGTGTGACCGGCACAGACATGAAGCTCGCGCTCCCTGCCAGTCCCGAG 294
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Db 295 ACCACCTGGACATGCTCCGCCACCTCTACACAGGGCTGCAGGTGGTCAGGGAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
Db 355 GAACTCACCTACCTGCCACCAATGCCAGCTGTCTCTCTGCAGGATATCCAGGAGGTG 414
QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTACGTGCTCATCGCTCACACCAAGTGAAGCAGGTCCCATCTGCAGAGGTGCGG 474
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QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
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QY 141 GlnLeuArgSerLeuThrGlnLeuLeuLysGlyValLeuIleGlnArgAsnProGln 160
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QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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Db 715 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAG 774
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QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 835 GCGGTGGCTGTGCCCGCTGCNAGGGGCACCTGCCACCTGACTGTGCTCATGAGCAGTGT 894
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheHis 260
Db 895 GCTGCGGCTGCACGGGCCCCCAAGCACTCTGACTGCTGGCTGCTCCACTTCAACCCAC 954
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QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
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QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
DB 2095 GGCTGCCCGCCGAGCAGAGAGCGCCCTCTGACGTTCATCATCTCTGCGGTGGTGGC 2154
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DB 2155 ATTCTGCTGCTGCTGCTTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCGACGAG 2214
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DB 2215 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGAAACGGAGCTGGTGGAGCGCGTG 2274
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DB 2275 ACACCTAGCGGAGCGATGCCAACACGAGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2334
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DB 2335 AGGAAGTGAAGTGTGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2394
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DB 2455 CCCAAAGCCAAAGAAATCTTAGAGAAAGCATACGTGATGCTGCTGGTGGGCTCCCCA 2514
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DB 3055 ATTGACTCTGAATGTCCGCCAAGATTCCCGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 3114
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
DB 3115 AGGAGCCCCAGCGCTTTTGTGTCATCCAGAATGAGGACTTGGGCCCGACGAGTCCCTTG 3174
QY 665 AspSerThrPheTyrArgSerLeuLeuAspAspMetGlyAspLeuValAspAla 684
DB 3175 GACAGCACCTTCTACCGCTCCTGCTGGAGGACATGACATGGGGACCTTGGTGGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3235 GAGGAGTATCTGTTACCCAGCAGGCGCTTCTTCTGTCCAGACCTTGCCTCCCGCGCTGGG 3294
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
DB 3295 GGCATGCTCCACACAGGACCGCAGCTCATCTACAGGAGTGGCGTGGGACCTTGACA 3354
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
DB 3355 CTAGGCTGGAGCCCTCTGAGAGGAGGCCCGCAGGTCTCCACTGGCACCTTCGAAGGG 3414
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
DB 3415 GCTGGCTCCGATGTATTTGATGTGACCTGGGAATGGGGGACAGAGGGCTGCAAGC 3474
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
DB 3535 CCCTCTGAGACTGATGGCTACGTTGCCCTCCCTGACTGACGCCCCCAGCCCTGATATGTG 3594
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
DB 3595 AACCCAGCAGATGTTCCGGCCCCAGCCCTTCCGCCCGAGAGGGCCCTCTGCTGCTGCC 3654
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
DB 3655 CGACCTGCTGGTGGCACTCTGGAAAGGCCCAAGACTCTCTCCCCAGGGAAGAATGGGGTC 3714
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
DB 3715 GTCAAGAGCTTTTTCCTTTGGGGTGGCTGGAGAACCCCCAGTACTTTGACACCCAG 3774
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
DB 3775 GGAGGAGTGGCCCTCAGCCCCCAGCCCTCTCTGCTGCTTCCAGCCAGCCTTCGACCACTC 3834
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
DB 3835 TATTACTGGGACCAGACCCACAGAGCGGGGGCTCCACCCAGCACCTTTCAAGGGACA 3894
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
DB 3895 CCTACGGCAGAAACCCAGAGTACTTGGGTCTGGACGTGCCAGTG 3939

RESULT 6

US-09-441-411-5

; Sequence 5, Application US/09441411

; Patent No. 6734172

; GENERAL INFORMATION:

APPLICANT: Scholler, Nathalie B.
APPLICANT: Disie, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 4473
TYPE: DNA
ORGANISM: Homo sapiens
US-09-441-411-5

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-441-411-5 (1-4473)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 235 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCCTGCCAGTCCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 295 ACCACCTGGACATGTCGCCACCTCTACAGGGCTGCCAGGTGGTGGAGGAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 355 GAACTCACCTACTGCCCCCAATGCCAGCTGTCTTCTCGAGGATATCCAGGAGGTG 414
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 415 CAGGGCTAGTGTCTATCGCTCACACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGGG 474
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
DB 475 ATTTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGACAAATGGA 534
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 535 GACCCCTGAAACAAATACCACTCTGTCAAGGGGCTCCCGAGAGGCTCGGGAGGCTG 594
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 595 CAGCTTCGAAGCTCACAGAGATCTTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG 654
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
DB 655 CTCTGTACAGACACGATTTTGTGGAAGGACATCTTCACAAGAACCAACAGCTGGCT 714
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 715 CTCACACTGATAGACACCAACCGCTCTCGGGCTTGCCACCTCTTCTCCGATGTGTAG 774
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 775 GGTCCCGCTGTGGGAGAGAGATTCTGAGGATTGTGCAGAGCTGCAGCGCACTGTCTCT 834
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysHisGlnGlnCys 240
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QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
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QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1435 GACCTCAGGCTCTCCAGAACCTGCAGTNAATCCGGGACAGNAATTCGCACAAATGGGCGC 1494
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DB 1555 CTGGGCACTGGACTGGCCCTCATCCACCATACACCCACCTCTGCTTGTGTGCACAGGTG 1614
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1675 GAGGACGAGTGTGTGGGAGGGCTGGCTGCCACCACTGCTGGCGCCGAGGGCACTGC 1734
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QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
2095 GGCTGCCGCCCGAGCAGAGAGCAGCCCTCTGAGCTCCATCTCTGCGGTGGTTGGC 2154
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2155 ATTCTGCTGCTGTGTCTTTGGGGTGGTCTTTGGGATCTCTATCAAGCAGCGCAGCAG 2214
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654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
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665 AppSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
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685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
3235 GAGGAGTATCTGTACCCAGCAGGGCTTCTCTGTCCAGACCTGCCCGCGCGCTGGG 3294
705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
3295 GGCATGGTCCACCACAGGCACCGCAGCTCATCTACCCAGGAGTGGCGTGGGACCTTGACA 3354
725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
3355 CTAGGCTGGAGCCCTCTGAAGAGGAGGCCCGCAGGTCTCTCACTGGCACCTCCGAGGG 3414
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885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaValGluAsnProGluTyrLeuThr 904
3835 TATTACTGGGACGAGACCCACAGAGCGGGGGCTCCACCCAGACCTTCAAGGAGACA 3894
905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
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RESULT 7

US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16

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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-811-115-2 (1-3768)

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QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrgingGlyCysGlnValValGlnGlyAsnLeu 60
DB 121 ACCACCTGGACATGCTCGCCACCTCTTACCAGGGCTGCCAGGTGGTGCAGGGAACCTG 180

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QY 81 GlnGlyTyrlleuValleuAlaHisAsnGlnValArgGlnValProleuGlnArgLeuArg 100
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QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
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QY 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuLeuIleGlnArgHengProGln 160
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QY 161 LeuCysTyrlleuAspThrIleLeuTyrlleuAspIlePheHisLeuAsnGlnLeuAla 180
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DB 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAAG 600

QY 201 GlySerArgCysTrpGlyGluSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 601 GCGTCCCGCTGTGGGAGAGAGATTTGAGGATTTGTGAGGCTGTGAGGCTGACGCGGCTGTCTGT 660

QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
DB 661 GCGGTGGCTGTGCCCGCTGCAAGGGGCGCACCTGCCCACTGCTGTGCTGAGCAGTGT 720

QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrlleuThrAspThrPheGlu 280
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QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerIysProCysAlaArg 340
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QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
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QY 401 GluThrLeuGluGluIleThrGlyTyrlleuTyrlleuSerAlaTrpProAspSerLeuPro 420
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QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1261 GACCTCAGCGCTTCTCCAGAACCTGCAAGTAATCCGGGAGCAATTTGACAAATGGCGCC 1320

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DB 1321 TACTCGCTGACCTTCAAGGGCTGGGCTATCAGCTGGCTGGGGCTGCGCTCACTAGGGAA 1380

QY 461 LeuGlySerGlyLeuAlaLeuIleHisIleAsnThrHisLeuCysPheValHisThrVal 480
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QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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DB 1561 TGGGCTCCAGGGCCACCCAGTGTGTCACTGCAGCCAGTTCTTTCGGGGCCAGGAGTGC 1620

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DB 1741 GCTGACAGTGTGTGGCTTGTGCCCATATAGGAGCCCTTCTTCTGCGTGGCCGCTGC 1800

QY 601 ProSerGlyValLysProAspLeuSerTyrlleuMetProIleTrpLysPheProAspGlu 620
DB 1801 CCCAGCGGTGTGAACCTGACCTCTCTACATGCGCATCTGGAAGTTTCCAGATGAGGAG 1860

QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
DB 1861 GCGCATGCCAGCTTGGCCCCATCAACTCACTCCTCTGTGTGGAGCTGTGATGACAAAG 1920

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QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
DB 1921 GGCTGCCCCCGCAGCAGAGAGCAGCCCTCTGACGTCCATCGTCTCTGGCGTGGTGGC 1980
QY 653 ----- 653
DB 1981 ATTCTGCTGGTCTGGTCTTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040
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DB 2041 AAGATCCGGAAGTACAGATGCGGAGACTGCTGCAAGAAACGGAGCTGGTGGAGCCGCTG 2100
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DB 2101 ACACCTAGCGGAGCGATGCCCAACAGCGCGCAGATCGGATCCTGAAAGAGACGGAGCTG 2160
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DB 2161 AGGAAGGTGAAGTGGTGGATCTGGCGCTTTTGGCACAGTCTACAAAGGCATCTGGATC 2220
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DB 2221 CCTGATGGGAGAAATGAAATTCAGTGGCCATCAAAGTGTGAGGGAACACATCC 2280
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DB 2281 CCCAAAGCCAAAGAAATCTTAGAGAGCATACGTGATGCTGTGTGGGCTCCCCA 2340
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DB 2341 TATGTCCTCCGCCCTCTGGGCATCTGCTGACATCCACGGTGAGCTGGTGACACAGTT 2400
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DB 2401 ATGCCCTATGGCTGCTCTTAGACCATGTCGGGAAACCGCGGACGCTGGGCTCCAG 2460
QY 653 ----- 653
DB 2461 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGTACCTGGAGGATGTGCGG 2520
QY 653 ----- 653
DB 2521 CTCGTACACAGGACTTTGGCCGCTCGGAAGTCTGTCGAAGTCCCAACCATGTCAA 2580
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DB 2581 ATTACAGACTTCGGGCTGGCTCGGCTGCTGGACATTGACGAGACAGGTACCATGCAGAT 2640
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DB 2641 GGGGGCAAGTGCCCATCAAGTGGATGGGCTGGAGTCCATTCTCCGCGCGGTTTCACC 2700
QY 653 ----- 653
DB 2701 CACCAGATGATGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGATTTTGGGGCC 2760
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DB 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGCTGCTCAAAATGTTGGATG 2880
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DB 2881 ATTGACTCTGAATGTGCGGCAAGATTCCGGGAGTTGGTGTCTGAAATTTCTCCCGCATGGCC 2940
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QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 694

DB 3001 GACAGCACCTTTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT 3060
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DB 3061 GAGGAGTATCTGGTACCCAGCAGGGCTTCTTCTGTCTCAGACCTGCCCGGGCGCTGGG 3120
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DB 3121 GGCATGGTCCACACAGGACCGCAGCTCATCTACCGAGTGGCGGTGGGACCTTGACA 3180
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
DB 3181 CTAGGGCTCGAGCCCTCTGAAGAGGAGGCCCCAGGTCTCCACTGCGACCCCTCCGAAGGG 3240
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyGlyLeuGlnSer 764
DB 3241 GCTGGCTCCGATGTATTGATGGTGACCTGGGAATGGGGGCGAGCCGAGGGCTGCAAGC 3300
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
DB 3301 CTCCCCACATGACCCCGCAGCCCTCTACAGCGGTACAGTGAGGACCCACAGTACCCCTG 3360
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
DB 3361 CCCTCTGAGACTGATGGTACGTGCCCCCTGACCTGCGAGCCCGCAGCCTGAATATGTG 3420
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
DB 3421 AACCAGCAGATGTTGGGCCCGCCAGCCCTTGGCCCCGAGAGGGCCCTCTGCTGCTGCC 3480
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
DB 3481 CGACCTGCTGGTGCCACTCTGGAAGGGGCCAAGACTCTCTCCCGAGGAGGAATGGGGTC 3540
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
DB 3541 GTCAAAGACGTTTTTGGCCTTGGGGGTGCGTGGAGAACCCCGAGTACTTGACACCCAG 3600
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
DB 3601 GGAGGAGCTGCCCTCAGCCCGCCCTCTCTGCTGCTTCCAGCCAGCCTTCGACCACTC 3660
QY 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
DB 3661 TATTACTGGGACGAGCACCACAGAGCGGGGGCTCCACCCAGCACCTTCAAAGGACA 3720
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
DB 3721 CCTACGGCAGAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3765

RESULT 8

US-08-229-515A-9
; Sequence 9, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER:  US/08/229,515A
/   FILING DATE:        19 APR 1994
/   CLASSIFICATION:     435
/   ATTORNEY/AGENT INFORMATION:
/     NAME:  PERRYMAN, DAVID G
/     REGISTRATION NUMBER: 33,438
/     REFERENCE/DOCKET NUMBER: 1414,608
/   TELECOMMUNICATION INFORMATION:
/     TELEPHONE: 404-688-0770
/     TELEFAX: 404-688-9880
/   INFORMATION FOR SEQ ID NO: 9:
/     SEQUENCE CHARACTERISTICS:
/       LENGTH: 4530 base pairs
/       TYPE: nucleic acid
/       STRANDEDNESS: single
/       TOPOLOGY: linear
/   US-08-229-515A-9

Alignment Scores:
Pred. No.: 0          Length: 4530
Score: 4892.00        Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 1 Gaps: 1

US-09-493-480-6 (1-919) x US-08-229-515A-9 (1-4530)
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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 211 GCGAGCACCAAGTGTGCACCGCGCACAGACATGAAGCTCGGCTCCCTGCCAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 271 ACCACCTGGACATGCTCCGCCACCTCTACCAAGGTGCGAGGTGTCAGGTGTGTCAGGGAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 331 GAACTCACCTACCTGCTCCCAACCAATGCCAGCCTGTCTCTCTCCAGGATATCCAGAGGTG 390
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 391 CAGGGCTAGCTGCTCATCGCTCACACCAAGTGAGCAGGTCCCACTGCGAGAGGTGCGG 450
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QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 511 GACCCGCTGAACAATACCACTCCCTGTCCAGAGGGCTCCCGAGGAGCTGCGGAGCTG 570
QY 141 GlnLeuArgSerLeuThrGlnLeuLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 571 CAGCTTCGAAGCCTCACAGAGATCTTTGAAGAGGGGTCTTGTATCCAGCGGAACCCCGAG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
DB 631 CTCCTGTACAGGACACAGATTTTGTGGAAGGACATCTTCACAGAACCAACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCGACCCCTGTCTCCGATGTGTAAG 750
QY 201 GlySerArgCysTrpGlyGlnSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 751 GGCCTCCCGCTGCTGGGGAGAGATTTCTGAGGATTTGTACAGAGCTGACGCGCATCTGTCTGT 810

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QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
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QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 871 GCTGCCGCTGCACGGGCCCAAGCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 931 AGTGGCATCTGTGAGCTGCACCTGCCCGAGCCCTGGTCACTACCAACACAGACAGCTTTGAG 990
QY 281 SerMetProAsnProGluGlyValArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 1051 TACAACCTACCTTTCTACGGACGCTGGGATCTTGACACCTCGTCTGCCCTGCACAAACCA 1110
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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DB 1171 GTGTCTATGTCTGGGCATGGAGCACCTTGCAGAGAGGTGAGGGCAGTTACCACTGCCAAT 1230
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DB 1351 GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGCGCGGACAGCTGCTGCT 1410
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DB 1411 GACCTCAGCGCTTCTCCAGAACCTGCAGTAATCCCGGGACGAAATCTGCACAAATGGCGCC 1470
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QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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DB 1711 TGGGGTCCAGGGCCCAACCCAGTGTGTAACCTGCAGCCAGTTCTTCTCGGGGCCAGGAGTGC 1770
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1951 CCCAGCGGTGAAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 2010
621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
2011 GGGCGATGCCAGCGCTTGGCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAA 2070
641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
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685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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3271 GGCATGGTCCACCACAGGACCCGACGCTCATCTACCAGGAGTGGCGTGGGGACCTTGACA 3330
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3331 CTAGGCGCTGGAGCCCTCTGAAGAGGAGGCCCCCGAGGTCTCCACTGGCACCTCCGAAGG 3390
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3811 TATTACTGGAGCCAGACCCACCCAGAGCGGGGGCTCCACCCAGCACCTTTCAAAGGAGCA 3870
905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
3871 CCTACGGCAGAGAAACCCAGAGTACTTGGGTCTGGACGTGCCAGTG 3915

RESULT 9

US-08-645-865-9
; Sequence 9, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

/ ADDRESSES: NEEDLE & ROSENBERG PC
 / STREET: 127 Peachtree Street, Suite 1200
 / CITY: Atlanta
 / STATE: Georgia
 / COUNTRY: usa
 / ZIP: 30303
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/645,865
 / FILING DATE: 14 MAY 1996
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: PERRYMAN, DAVID G
 / REGISTRATION NUMBER: 33,438
 / REFERENCE/DOCKET NUMBER: 1414.608
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 404-688-0770
 / TELEFAX: 404-688-9880
 / INFORMATION FOR SEQ ID NO: 9:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 4530 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / US-08-645-865-9

Alignment Scores:

Pred. No.: 0 Length: 4530
 Score: 4892.00 Matches: 918
 Percent Similarity: 73.13% Conservative: 0
 Best Local Similarity: 73.15% Mismatches: 1
 Query Match: 96.34% Indels: 336
 DB: 1 Gaps: 1

US-09-493-480-6 (1-919) x US-08-645-865-9 (1-4530)

QY 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
 DB 151 ATGGAGCTGGCGGCTTGTGGCGCTGGGGCTCTCTCGCCCTCTTGGCCCGCGGAGCC 210
 QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 DB 211 GCGAGACCAAGTGTGCACCGGCACAGACATGAAGCTCGGCTCCCTGCCAGTCCCCGAG 270
 QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 DB 271 ACCACCTGGACATGCTCCGCCACCTCTACCAAGGCTGCCAGTGGTGCAGGGAAACCTG 330
 QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
 DB 331 GAACTCACCTACTGCCCCACCAATGCCAGCTGTCTCTCCAGGATATCCAGAGGTG 390
 QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
 DB 391 CAGGGCTAGTGCTCATCGCTCACAAACCAAGTGAGCGAGTCCCACTGCAGAGGCTGCGG 450
 QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
 DB 451 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGCCCTGCCAGTGGAGTGA 510
 QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 DB 511 GACCGGCTGAACAATACCACTCTTTGAGGACAACTATGCCCTGCCCTGCCAGGCTGCGG 570
 QY 141 GlnLeuArgSerLeuThrGlnIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
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DB 631 CTCTGCTACCAAGCACCATTTTGTGGAAGGACATCTTCCACAAGACAACACGCTGGCT 690
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 DB 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAAG 750
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 QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
 DB 1171 GTGTGCTATGTCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACCAGTGCCAA 1230
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 DB 1231 ATCCAGGAGTTTGTGCTGGCTGCAAGAAGATCTTTGGGAGCTTGGCATTTTGTCCGAGAG 1290
 QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
 DB 1291 TTTGATGGGGACCCAGCCCTCCAACTGCCCCGCTCCAGCCAGAGCAGCTCCAGTGT 1350
 QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
 DB 1351 GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGCGCGACAGCTGCT 1410
 QY 421 AspLeuSerValPheGlnAsnLeuValIleArgGlyArgIleLeuHisGlnGlyAla 440
 DB 1411 GACCTCAGCGCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTTCTGCACAAATGGCG 1470
 QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
 DB 1471 TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGGCTCACTGAGGGA 1530
 QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
 DB 1531 CTGGCAGTGGACTGGCCCTCATCCACCAATACCCACCTCTGCTTCTGTCACACGGGTG 1590
 QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
 DB 1591 CCCTGGGACCAAGCTCTTTCCGAACCCGACCAAGCTCTGCTCTCCACTGCCAACCGGCA 1650
 QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
 DB 1651 GAGGACGAGTGTGTGGGCGAGGGCTTGGCTGCCACACAGCTGTGGCCCGAGGCACTGC 1710
 QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540

Db	1711	TGGGGTCAGGGCCACCAGTGTGTCAACTGCGAGCAGTTCTTCGGGGCCAGGAGTGC	1770
Qy	541	ValGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaAatHisCys	560
Db	1771	GTGGAGAAATGCCGAGTACTGACGGGCTCCACAGGAGATATGTGAATGCCAGGCACTGT	1830
Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
Db	1831	TTGCGGTGCCACCTGTAGTGTACGCCACAGAAATGGCTCAGTGACCTGTGTTGGACCGGAG	1890
Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaAatCys	600
Db	1891	GCTGACCAAGTGTGGCTGTGCCCACTATAGACCCCTCCCTTCTGCGTGGCCCGCTGC	1950
Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu	620
Db	1951	CCCAGCGGTGGAACCTGACCTCTCTACATGCCATCTGGAAGTTTCCAGATGAGGAG	2010
Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
Db	2011	GGCGCATGCCAGCCTTGCCTCATCACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG	2070
Qy	641	GlyCysProAlaGlnArgAlaSerProLeuThrSer-----	653
Db	2071	GGCTGCCCCCGAGCAGAGAGCCGCTCTGACGTCCATCGTCTCTGCGGTGGTGGC	2130
Qy	653	-----	653
Db	2131	ATTCTGTGTGCGTGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCAGCGCAGCAG	2190
Qy	653	-----	653
Db	2191	AAGATCCGGAAGTACACGATGCGGAGACTGTCGAGGAAACGGAGCTGGTGGAGCCGCTG	2250
Qy	653	-----	653
Db	2251	ACACCTAGCGAGGATGCCCAACCGAGCGCAGATGCGGATCCTGTAAGAGACGGAGCTG	2310
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Db	2311	AGGAAGTGAAGTGTGTGGATCTGGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC	2370
Qy	653	-----	653
Db	2371	CCTGATGGGAGAAATGTGAAAATTTCCAGTGCCCATCAAAGTGTGAGGGAAAAACACATCC	2430
Qy	653	-----	653
Db	2431	CCCAAGCCAAAGAAATCTTAGCGAAGCATACGTGATGGTGTGGGTCCCCCA	2490
Qy	653	-----	653
Db	2491	TATGTCTCCGCTTCTGGGCATCTGCTGCATCCACGGTGCAGCTGGTGACACAGCTT	2550
Qy	653	-----	653
Db	2551	ATGCCCTTAGGCTGCTTTAGACCATGTCGGGAAACCGCGAGCCCTGGGCTCCAG	2610
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Db	2611	GACCTGTGAATGTTATGCAGATTGCCAAGGGATGAGTACTCTGGAGGATGTGCGG	2670
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Db	2671	CTCGTACACAGGACTTGGCGCTCGGAACGTGTGTCAGAGTCCCAACCATGTCAAA	2730
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Db	2791	GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTTCTCGCGCGGCTTCAAC	2850
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Qy	653	-----	653
Db	2911	AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGTCTGGAAGAGGGGAGCGG	2970
Qy	653	-----	653
Db	2971	CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGGTCAAAATGTTGGATG	3030
Qy	653	-----	653
Db	3031	ATTGACTCTGAATGTCCGCCAAGATCCCGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC	3090
Qy	654	-----GlnAsnGluAspLeuGlyProAlaSerProLeu	664
Db	3091	AGGACCCCCAGCGCTTTGTGTCATCCAGAATGAGGACTTGGGCCCGCAGCTCCCTTG	3150
Qy	665	AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	3151	GACAGCACCTTTACCGCTCACTGCTGGAGGACATGACATGGGGACCTTGGTGGATGCT	3210
Qy	685	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	704
Db	3211	GAGGAGTATCTGTGTACCCAGCAGGCTTCTTCTGTCCAGACCTGCCCCGGCGCTGGG	3270
Qy	705	GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr	724
Db	3271	GGCATGTCCACACAGGACCGCAGCTCATCTACCAGGAGTGGCGTGGGACCTGCACA	3330
Qy	725	LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly	744
Db	3331	CTAGGCTGGAGCCCTCTGAGAGGAGGCCCCAGGTCTCCACTGGCACCTCTCGAAGGG	3390
Qy	745	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer	764
Db	3391	GCTGGCTCCGATGATTTGATGTGACCTGGGAATGGGGACGCCAAGGGGCTGCAAGC	3450
Qy	765	LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu	784
Db	3451	CTCCCCACACATGACCCCGCTCTACAGCGGTACAGTGAGGACCCACAGTACCCCTG	3510
Qy	785	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal	804
Db	3511	CCCTCTGAGACTGATGGCTACGTTGCCCTCCCTGACCTGCGAGCCCCCAGCTGTAATATGTG	3570
Qy	805	AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla	824
Db	3571	AACCCAGCAGATGTTCCGGCCCCAGCCCCCTTCCGCCCGAGAGGGCCCTCTGCTGCTGCC	3630
Qy	825	ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal	844
Db	3631	CGACCTGCTGGTGCCACTCTGGAAGGGGCCAAGACTCTCTCCCCAGGAGAATGGGGTC	3690
Qy	845	ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln	864
Db	3691	GTCAAGAGCTTTTTCCTTTGGGGGTGCGGTGGAGAACCCCGAGTACTTTGACACCCAG	3750
Qy	865	GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu	884
Db	3751	GGAGGAGCTGCCCTCAGCCCCCAGCTCTCTCTGCTTCCAGCCCGCTTCCGACCACTC	3810
Qy	885	TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr	904
Db	3811	TATTACTGGAGCAGACCCACAGAGCGGGGGCTCCACCCAGCACCTTTCAAAGGACA	3870
Qy	905	ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal	919
Db	3871	CTTACGGCAGAGAACCCAGAGTACTTGGGTCTGGAGCTGCCAGTG	3915

391	Db	CAGGGCTACGTGCTCATCGCTCACACCAAGTCAGGAGGTCCTCCACTGTCAGAGGCTGCGG	450
101	Qy	IlleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
451	Db	ATTGTGCGAGGACACCCAGCTCTTTTGAGGACAACTATGCCCCTGGCCGTGTAGACAATGGA	510
121	Qy	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
511	Db	GACCCGCTGAACAAATACCAACCCCTGTGCACAGGGGCTCCCCAGAGAGCCCTGCGGGAGCTG	570
141	Qy	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
571	Db	CAGCTTCGAAGCCTCACAGAGATCTTTAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG	630
161	Qy	LeuCyTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
631	Db	CTCTGCTACAGGACACGATTTGTGGAGGACATCTTCACAGAACAACACAGCTGGCT	690
181	Qy	LeuThrLeuIleAspThrAsnArgSerArgAlaCyHisProCysSerProMetCysLys	200
691	Db	CTCACACTGATACACCAACCGCTCTCGGGCTGCGCACCCCTGTTCTCCGATGTGTAAG	750
201	Qy	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
751	Db	GGCTCCCGCTGCTGGGGAGAGAGTCTCTAGGATTTGTACAGCCTGACGGCGCACTGCTGT	810
221	Qy	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCyHisGluGlnCys	240
811	Db	GC CGGTGGCTGTGCCCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT	870
241	Qy	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
871	Db	GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGCTGGCCCTGCCCTTCAACCAAC	930
261	Qy	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
931	Db	AGTGGCATCTGTGAGCTGCACCTGCCAGCGCTGTGTCACCTTACAACACAGACACGTTTGAG	990
281	Qy	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
991	Db	TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGGGCCAGCTGTGTGACTGCTGTCCC	1050
301	Qy	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
1051	Db	TACAACTACTTCTACGGACGFGGGATCTGTGACCCCTGTCTGCCCCCTTGCACAACCAA	1110
321	Qy	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
1111	Db	GAGGTACACAGCAGAGATGGAAACACACAGCGGTGTGAAGTGCAGCAAGCCCTGTGCCCGA	1170
341	Qy	ValCyTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
1171	Db	GTGTGCTATGGTCTGGGCATGGAGCACTTGGAGAGGTGAGGGCAGTTACCACTGCCAAT	1230
361	Qy	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
1231	Db	ATCCAGAGTTTCTGGCTGCAAGAAAGATCTTTGGGAGCCTTGGCAATTTCTGCGGAGAGC	1290
381	Qy	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
1291	Db	TTTGATGGGGACCCAGCCTCCAACTGCCCCCTCCAGCGAGAGCAGCTCCAAGTGTGTT	1350
401	Qy	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
1351	Db	GAGACTCTGGAAGAGATCACAGGTACCTATATCATCTCAGCATGGCCGGAAGCCTGCCT	1410
421	Qy	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
1411	Db	GACCTCAGCGCTCTTCAGAAACCTGCAAGTAATCCGGGGACGAATTTCTGCACAATGGGCC	1470
441	Qy	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
1471	Db	TACTCGCTGACCCCTGCAAGGCTGGGCATCAGCTGCTGGGGCTGGCTCCTCCTGAGGGGA	1530

QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
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DB 3211 GAGGAGTATCTGTGTACCCAGCAGGGCTTCTCTGTCCAGACCTTGGCCCGGGCGCTGGG 3270
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RESULT 11
US-09-527-487-1
; Sequence 1, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)...(3915)
US-09-527-487-1

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-527-487-1 (1-4530)

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Db 211 GCGAGACCCAAAGTGTGCACCGGCACAGACATGAAGCTCGGCTCCTCGCCAGTCCCGAG 270
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
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Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
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Qy 81 GlnGlyTyrValIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGCTAGTGTCTATCGCTCACACCAAGTGAGCAGGTCCCACTGCAGAGGCTGCGG 450
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1471 TACTCGCTGACCTTCAGAGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGAA 1530
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1531 CTGGCAGTGGACTGGCCCTCATCCACCAACCAACCCCTCTGCTTGTGTCACACGCTG 1590
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1591 CCCTGGGACCAAGCTCTTTGGAAACCCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1650

QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1711 TGGGGTCCAGGGCCACCCAGTGTGTCACTGACGCCAGTTCCTTTCGGGGCCAGGAGTGC 1770
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1771 GTGGAGGAATGCCGAGTACTGCAAGGGCTCCCCAGGAGTATGTGAATGCCAGGCACTGT 1830
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1831 TTGCCGTGCCACCTGAGTGTCTAGCCCCCAGAATGGGTCACTGACCTGTTTTGGACCGGAG 1890
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
DB 1891 GCTGACAGTGTGTGGCTGTGCCCACTATAGGACCCCTCCCTTCTGGGTGGCCGCTGC 1950
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
DB 1951 CCCAGCGGTGAAACCTGACCTCTCTACATSCCCATCTGGGAATTTCCAGATGAGGAG 2010
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
DB 2011 GGGCGCATGCCAGCTTGGCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG 2070
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
DB 2071 GGCTGCCGCCGAGCAGAGAGCCGCTCTGACGTCCATCTCTCTGCGGTGGTTGGC 2130
QY 653 ----- 653
DB 2131 ATTCTGCTGCTGCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCGAGCAG 2190
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DB 2191 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCGCGTG 2250
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DB 2251 ACACCTAGCGGAGCGATGCCAACCGAGCGCAGATGCGGATCTGAAAGACGCGAGCTG 2310
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DB 2311 AGGAAGGTGAAGTGTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2370
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DB 2431 CCCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGCTGGTGGGCTCCCCA 2490
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DB 2671 CTCGTACACAGGACTTGGCCGCTCGGAAGCTGCTGGTCAAGAGTCCCAACCATGTCAAA 2730
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DB 2731 ATTACAGACTTCGGGCTGGCTCGGCTGCTGGACATTTACGACAGACAGAGTACCATGCAGAT 2790
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QY 653 ----- 653
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DB 3031 ATTGACTCTGAATGTCCGCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 3090
QY 654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
DB 3091 AGGGACCCCCAGCGCTTTGTGGTCAATCCAGAATGAGGACTTGGGCCCGCAGCTCCCTTG 3150
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
DB 3151 GACAGACCTTTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGTGGTGGATGCT 3210
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3211 GAGGATATCTGGTACCCCGCAGCAGCGCTTCTTCTGTCCAGACCCTGCCCGCGCTGGG 3270
QY 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
DB 3271 GGCATGGTCCACACAGGACCGCAGCTCATCTACAGAGTGGCGGTGGGAGCCTTGACA 3330
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
DB 3331 CTAGGGCTGGAGCCCTCTGAGAGGAGGCCCCCAGGTCTCCACTGAGCACCTCCGAAGGG 3390
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaLysGlyLeuGlnSer 764
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DB 3511 CCTCTGAACATGATGGCTACGTGTGCCCCCTGACCTGACGCCCCAGCCCTGATATGTG 3570
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QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
DB 3631 CGACCTGCTGGTGCCTCTCTGGAAAGGGCCAAAGACTCTCTCCCGCAGGGAATGGGGTC 3690
QY 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
DB 3691 GTCAAGACGTTTTTGCCTTTGGGGTGCCTGGAGAACCCCGACTCTTGACACCCAG 3750
QY 865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 884
DB 3751 GGAGGAGCTGCCCTCAGCCCCCCTCTCTCTGCTTCCAGCCCGCAGCTTCGACCACTC 3810
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904

Db 3811 TATTACTGGACAGCACCACAGAGCGGGGGCTCCACCAGCACCTTCAAAGGGACA 3870

Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
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Db 3871 CCTACGGCAGAAACCAGAGTACCTGGGTCTGGACGTGCCAGTG 3915

RESULT 12

US-09-877-177A-11

; Sequence 11, Application US/09877177A

; Patent No. 6582919

; GENERAL INFORMATION:

; APPLICANT: K. Danenberg

; TITLE OF INVENTION: Method of determining Epidermal Growth

; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression

; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival

; FILE REFERENCE: 11220/120

; CURRENT APPLICATION NUMBER: US/09/877,177A

; CURRENT FILING DATE: 2001-06-11

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 4530

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-877-177A-11

Alignment Scores:

Pred. No.:	0	Length:	4530
Score:	4892.00	Matches:	918
Percent Similarity:	73.15%	Conservative:	0
Best Local Similarity:	73.15%	Mismatches:	1
Query Match:	96.34%	Indels:	336
DB:	4	Gaps:	1

US-09-493-480-6 (1-919) x US-09-877-177A-11 (1-4530)

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Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40

Db 211 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTCGGCTCCCTGCCAGTCCCGAG 270

Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnValAsnLeu 60

Db 271 ACCACCTGGACATGCTCCGCCACCTCTACCAAGGCTGCCAGGTGTGAGGGAACCTG 330

Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80

Db 331 GAACTCACCTACCTGCCACCAATGCCAGCCTGTCTCTCTCGAGGATATCCAGGAGGTG 390

Qy 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100

Db 391 CAGGGCTACGTGCTCATCGCTCACACCAAGTGAGGCAGGTCCCATCGCAGAGGTGCGG 450

Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120

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Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140

Db 511 GACCCGCTGAACAATACCAACCCCTGTGCACAGGGGCTCCCGAGGAGGCTGGGGAGCTG 570

Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160

Db 571 CAGCTTCGAAGCTCACAAGATCTTTGAAGAGGGGTCTTGAATCCAGCGGAACCCCGAG 630

Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLeuAsnGlnLeuAla 180

Db 631 CTCTGCTACGAGACACGATTTTGTGGAAGGACATCTTCCAAAGAACCAACAGCTGGCT 690

Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200

Db 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGAAG 750

Qy 201 GlySerArgCysTrpGlySerSerGluAspCysGlnSerLeuThrArgThrValCys 220

Db 751 GGTCCCGCTGCTGGGGAGAGATTCTGAGGATTCTGAGAGCTGACGCGCACTGTCTGT 810

Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240

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Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280

Db 931 AGTGGCATCTGTGAGCTGACTGCCCGAGCCCTGGTGCATCAACACACAGACACGTTT 990

Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300

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Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360

Db 1171 GTGTCTATGTCTGGGCATGGAGCATTGGCAGAGGTGAGGGCAGTTACCAAGTGCCAT 1230

Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380

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Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400

Db 1291 TTTGATGGGGACCCAGCCTCCAAACACTGCCCGCTCCAGCCACAGCAGCTCCAAGTGT 1350

Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420

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Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460

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Db 1531 CTGGCAGTGGACTGGCCCTCATCCACCATTAACACCCACCTCTGCTTCGTGACACGGTG 1590

Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500

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Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520

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Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560

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Db TTGCGGTGCCACCTGAGTGTGACGCCCCAGAAATGGCTCAGTGACCTGTTTGGACCGGAG 1890
Qy 581 AlaspGlnCysValAlaCysAlaHisTyrIlyAspProPheCysValAlaArgCys 600
Db 1891 GCTGACCAGTGTGTGGGCTGTGCCCACTATAAGGACCCTCCCTTCTGCGTGGCCGCTGC 1950
Qy ProSerGlyValIlyProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
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Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
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Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 2071 GGCTGCCCGCCGAGCAGAGCCAGCCCTCTGACGTCCATCGTCTCTGCGGTGGTTGGC 2130
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Db 2131 ATTCTGCTGTCGTGTCTTGGGGTGGTCTTTGGGATCTCTCAAGCGACGCGACAG 2190
Qy 653 653
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Db 2251 ACACCTAGCGGCGGATGCCCAACCGCGCGAGATGCGGATCTCTGAAAGAGACGGAGCTG 2310
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Db 2371 CCTGATGGGGAATGTGAAATTTCCAGTGGCCATCAAAAGTGTGAGGGAACACATCC 2430
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Qy 653 653
Db 2671 CTCGTACACAGGACTTTGGCGCTTCGGAACGTGTGTGTCAGAGTCCCAACCATGTCAAA 2730
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Db 2731 ATTACAGACTTCGGGCTGGCTCGGCTGCTGACATTGACGACAGAGTACCATGCAGAT 2790
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Db 2791 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTTCTCCCGCGGCTTCAAC 2850
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Db 2851 CACCAGAGTATGTGTGAGTATTGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2910

RESULT 13

US-09-811-115-1

; Sequence 1, Application US/09811115

; Patent No. 6632979

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Qy 653 653
Db 3031 ATTGACTCTGAATGTGCGCCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC 3090
Qy 654 654
Db 3091 AGGGACCCCGCGCTTTGTGGTCATCCAGAAATGAGACTTGGGCCCGCAGCAGTCCCTTG 3150
Qy 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3151 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGATGCT 3210
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3211 GAGGATATCTGTATACCCAGCAGGGCTTCTTGTCTCCAGACCTGCCCCGGGCGCTGG 3270
Qy 705 GlyMetValHisHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
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Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
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Db 3511 CCCTCTGAGACTGATGGCTACGTTGCCCTGACCTGCAGCCCCCAGCCCTGAATATGTG 3570
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Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3631 CGACCTGCTGGTCCACTCTGGAAGGGGCCCAAGACTCTCTCCCGCAGGAAGATGGGGTC 3690
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3691 GTCAAGAGCGTTTTTGGCTTTGGGGTGGCGTGAGAAACCCCGAGTACTTTGACACCCAG 3750
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Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3811 TATTACTGGGACCGAGCCACCCAGAGCGGGGGCTCCACCCAGCACCTTCAAAGGACA 3870
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Db 3871 CCTACGCGCAGAGAACCCAGAGTACCTGGGTCTGGAGCTGCGAGT 3915


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/ GENERAL INFORMATION:
/ APPLICANT: Erickson, Sharon
/ APPLICANT: Schwall, Ralph
/ APPLICANT: King, Kathleen
/ TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
/ FILE REFERENCE: GENENT.034A
/ CURRENT APPLICATION NUMBER: US/09/811,115
/ CURRENT FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/189,844
/ PRIOR FILING DATE: 2000-03-16
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 9274
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Vector Sequence
US-09-811-115-1

Alignment Scores:
Pred. No.: 0 Length: 9274
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-811-115-1 (1-9274)
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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
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DB 1851 ACCCACTGGACATGCTCCGCCACCTCTACCAAGGCTGTCAGGTGTGAGGAAACCTG 1910
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 1911 GAACTCACCTACCTGCCCAATGCCAGCTGCTCTCTCCAGGATATCAGGAGGTG 1970
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 1971 CAGGGCTACGCTGCTCATCGCTCACAAACCAAGTGAGGAGGTCTCCACTGCAGAGGCTGCGG 2030
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
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DB 2211 CTCCTGTACAGACACAGATTTTGTGAAGGACATCTTCCAAAGAACCAACAGCTGGCT 2270
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DB 2331 GGCCTCCGCTGCTGGGGAGAGAGTTCTGAGGATTTGTAGAGCTTGTAGAGCTTGACGGCCTCTGTCTGT 2390
QY 221 AlaGlyGlyCysAlaArgCysGlyProLeuProThrAspCysCysHisGluGlnCys 240
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DB 2451 GCTGCCGGCTGCACGGGCCCAAGCACCTGACTGCTGCTGGCTGCTCCACTTCAACCCAC 2510
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QY 281 SerMetProAsnProGluGlyValArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 2751 GTGTCTATGTCTGGGCATGGAGCACCTTGCAGAGGTGAGGGCAGTTACCACTGCTGCTGCTG 2810
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 2811 ATCCAGGAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2870
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 2871 TTTGATGGGGACCCAGCTCCAAACCTGCCCGCTCCAGCCAGAGCAGCTCCCAAGTGTGT 2930
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
DB 2931 GAGACTCTGGAGAGAGATCACAGTTACTATATACATCTCAGCATGCGCCGAGCAGCTGCT 2990
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 2991 GACCTCAGCGCTTCCAGAACCTGCAAGTAATCCGGGAGCAGAAATTCGCACAAATGGCGC 3050
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 3051 TACTCGCTGACCCCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCTGCTGCTGCTGCTG 3110
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 3111 CTGGGCGAGTGGACTGGCCCTCATCCACCATATACACCCACCTCTGCTTCTGTCACACGGTG 3170
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 3171 CCCTGGGACCAAGCTCTTTCGGAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA 3230
QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 3231 GAGGACGAGTGTGGGGAGGGCTGGCCCTGCCACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 3290
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 3291 TGGGGTCCAGGGCCACCCAGTGTGTCAACTGCAGCCAGTTCTCTTCGGGGCCAGGAGTGC 3350
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 3351 GTGGAGGAATCCGAGTACTGCAGGGGTCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 3410
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 3411 TTGCCGTGCCACCTGAGTGTGTCAGCCCCAGAAATGGCTCAGTACCTGTGTGTCAGCCGGAG 3470
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QY 581 AlaAspGlnCysValAlaCysAlaHisTyrIleAspProProPheCysValAlaAArgCys 600
Db 3471 GCTGACCAAGTGTGGGCTGTGGCCACTATAAGACCCCTCCCTTCTCGTGGCCGCTGC 3530
QY 601 ProSerGlyValIleAspLeuSerTyrMetProIleTrpIlePheProAspGluGlu 620
Db 3531 CCAGCGGTGTGAACCTGACCTCTCTATGTCCTCCATCTGGAAGTTTCCAGATGAGGAG 3590
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
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Db 3651 GGCTGCCCCCGCAGCAGAGAGCCGCCCTCTGACGTCCATCGTCTCTGCGGTGGTTGGC 3710
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Db 4491 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTGGAAGGGGAGCGG 4550
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QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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RESULT 14

US-08-229-515A-14
; Sequence 14, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19

Db 1586 CACTGCTGGGGCCAGGGCCACCAGCTGTGTCAACTGCGAGTCATTTCCTTCGGGGCCAG 1645
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RESULT 15
 US-08-645-865-14
 ; Sequence 14, Application US/08645865
 ; Patent No. 5654406
 ; GENERAL INFORMATION:
 ; APPLICANT: RAZIUDIN
 ; APPLICANT: SARKAR, FAZLU H
 ; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
 ; TITLE OF INVENTION: NEOPLASTIC DISEASE
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: NEEDLE & ROSENBERG PC
 ; STREET: 127 Peachtree Street, Suite 1200
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: usa
 ; ZIP: 30303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/645,865
 ; FILING DATE: 14 MAY 1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PERRYMAN, DAVID G
 ; REGISTRATION NUMBER: 33,438
 ; REFERENCE/DOCKET INFORMATION: 1414.608
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-688-0770
 ; TELEFAX: 404-688-9880
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3955 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-645-865-14

Alignment Scores:

Pred. No.: 0 Length: 3955
 Score: 4134.00 Matches: 781
 Percent Similarity: 65.47% Conservatives: 42
 Best Local Similarity: 62.13% Mismatches: 96
 Query Match: 81.41% Indels: 338
 DB: 1 Gaps: 3

US-09-493-480-6 (1-919) x US-08-645-865-14 (1-3955)

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QY      903  GlyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
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Search completed: August 3, 2005, 12:58:29
Job time : 522.375 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 3, 2005, 12:38:09 ; Search time 1373.71 Seconds
(without alignments)
4329.948 Million cell updates/sec

Title: US-09-493-480-6
Perfect score: 5078
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Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
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-MAXLEN=2000000000 -MMAP=US09493480 @CGN 1.1616 @runat_02082005_152648_25157
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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4900	96.5	3768	9	US-09-765-973-1 Sequence 1, Appli
2	4900	96.5	3768	9	US-09-854-356-9 Sequence 9, Appli
3	4900	96.5	3768	9	US-09-930-125-1 Sequence 1, Appli
4	4900	96.5	3768	16	US-10-313-644-1 Sequence 1, Appli
5	4900	96.5	4473	10	US-09-441-411-5 Sequence 32, Appli
6	4900	96.5	4473	15	US-10-146-473-32 Sequence 44, Appli
7	4900	96.5	4473	15	US-10-207-655-44 Sequence 81, Appli
8	4900	96.5	4473	20	US-10-101-510-81 Sequence 5, Appli
9	4900	96.5	4473	20	US-10-762-128-5 Sequence 8, Appli
10	4900	96.5	4473	20	US-10-723-860-8 Sequence 5, Appli
11	4892	96.3	3768	9	US-09-811-123-8 Sequence 2, Appli
12	4892	96.3	3768	11	US-09-984-092-3 Sequence 3, Appli
13	4892	96.3	3768	18	US-10-280-576-3 Sequence 3, Appli
14	4892	96.3	3768	19	US-10-441-779C-3 Sequence 3, Appli
15	4892	96.3	3768	19	US-10-384-339C-52 Sequence 52, Appli
16	4892	96.3	3768	9	US-09-877-177-11 Sequence 11, Appli
17	4892	96.3	4530	15	US-10-177-293-125 Sequence 125, App
18	4892	96.3	4530	15	US-10-007-926A-119 Sequence 119, App
19	4892	96.3	4530	15	US-10-338-730-1 Sequence 1, Appli
20	4892	96.3	4530	15	US-10-101-510-124 Sequence 124, App
21	4892	96.3	4530	17	US-10-116-275-131 Sequence 131, App
22	4892	96.3	4530	17	US-10-426-836-11 Sequence 11, Appli
23	4892	96.3	4530	17	US-10-272-437A-27 Sequence 27, Appli
24	4892	96.3	4530	17	US-10-117-937-595 Sequence 595, App
25	4892	96.3	4530	17	US-10-392-113-45 Sequence 45, Appli
26	4892	96.3	4530	17	US-10-159-563-208 Sequence 208, App
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32	4892	96.3	4530	21	US-10-794-514A-2 Sequence 2, Appli
33	4892	96.3	4530	21	US-10-871-708-18 Sequence 18, Appli
34	4892	96.3	4530	24	US-11-067-064-595 Sequence 595, App
35	4892	96.3	4642	14	US-10-198-846-10896 Sequence 10896, A
36	4892	96.3	4642	9	US-09-811-123-7 Sequence 7, Appli
37	4892	96.3	9274	9	US-09-811-115-1 Sequence 1, Appli
38	4892	96.3	9274	10	US-09-971-392-70 Sequence 70, Appli
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41	4849	95.5	4543	9	US-10-723-860-4619 Sequence 329, App
42	4617.5	90.9	5125	20	US-10-794-514A-329 Sequence 331, App
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09765973
; Publication No. US20020039573A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmermann, Susan
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND
; TREATMENT OF HER-2neu ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.496
; CURRENT APPLICATION NUMBER: US/09/765,973
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768

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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-765-973-1

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Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 9 Gaps: 1

US-09-493-480-6 (1-919) x US-09-765-973-1 (1-3768)

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Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGAGCGTTTTTGGCTTTGGGGTGGCGTGAGAACCCCGAGTACTTGACACCCAG 3600
Qy 865 GlyGlyAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGTGGCCCTCAGCCCCCAGCCCTCTCTCTGCTTCCAGCCAGCCTTCGACACCTC 3660
Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACCGAGCCACCCAGAGCGGGGGCTCCACCAGCACCTTCAAAGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAAACCAGAGTACCTGGGTCTGGACGTGCCAGTG 3765

RESULT 2

US-09-854-356-9
; Sequence 9, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
; OTHER INFORMATION: human HER-2/neu protein
; NAME/KEY: misc.feature
; LOCATION: (1)..(1959)
; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
; NAME/KEY: misc.feature
; LOCATION: (2026)..(3765)
; OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
; NAME/KEY: misc.feature
; LOCATION: (2968)..(3765)
; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
; NAME/KEY: misc.feature
; LOCATION: (2968)..(3144)
; OTHER INFORMATION: preferred portion of the phosphorylation domain
; OTHER INFORMATION: (Delta PD) of human HER-2/neu
US-09-854-356-9

Alignment Scores:

Pred. No.: 0 Length: 3768
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 9 Gaps: 1

US-09-493-480-6 (1-919) x US-09-854-356-9 (1-3768)

QY	1	MetGluLeuAlaLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla	20
DB	1	ATGGAGCTGGCGGCTTGTGGCGCTGGGGGCTCCCTCGCGCTCTTGGCCCCCGGAGCC	60
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
DB	61	GGGAGACCACAGTGTGCACCGGCGACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG	120
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
DB	121	ACCCACCTGGACATGCTCCGCCACCTCTACCAAGGCTGCCAGGTGGTGCAGGGAACCTG	180
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80
DB	181	GAACCTCACCTAGCTGCCACCAATGCCAGCTGTCTTCTCCAGGATATCCAGAGGTG	240
QY	81	GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValArgGlnValProLeuGlnArgLeu	100
DB	241	CAGGGCTACGTGCTCATCGCTCACAAACCAAGTGAGGAGGTCCCACTGCAGAGGCTGCGG	300
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
DB	301	ATTGTGGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGCTAGACAAATGGA	360
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
DB	361	GACCGGCTGAACAATACCAACCCCTGTACAGGGGCTCCCCAGGAGGCTCGGGAGCTG	420
QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
DB	421	CAGCTTCGAAGGCTCACAGAGATCTTGAAGAGGGGCTTTCATCAGCGGAACCCCGAG	480
QY	161	LeuCysThrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
DB	481	CTCTGCTACGAGACACAGATTTTGTGGAAGGACATCTCCACAGAACACACAGTGGCT	540
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	541	CTCACACTGATAGACACCAACCGCTCTCGGGCTCGCCACCCCTGTCTCCGATGTGAAG	600
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
DB	601	GGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTGTACAGAGCTTGACGGCGACTGTCTGT	660

QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
DB	661	GCCGCTGGCTGTGCCCGCTGCAAGGGCCACTGCCCACTGCTGCTGCCATGAGCAGTGT	720
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	721	GCTGCGGCTGCACGGGCCCAAGCACTCTGACTGCTGGCTGCTCCACTTCAACCAAC	780
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
DB	781	AGTGCGATCTGTGAGCTGCATGCCAGCCCTGGTGCCTACCAACACACACACAGTTT	840
QY	281	SerMetProAsnProGluGlyValArgTyrThrPheGlyAlaSerCysValThrAlaCys	300
DB	841	TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGGGCCAGCTGTGTGACTGCTGTC	900
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	901	TACAACTACCTTTCTACGGAGCTGGGATCCTGCACCCCTCGTGGCCCCCTGCACAA	960
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
DB	961	GAGGTGACAGCAGAGATGGAAACACAGCGGTGTGAAGTGCAGCAAGCCCTGTGCCCA	1020
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1021	GTGTGCTATGGTCTGGGCATGGAGCATTGGCAGAGGTGAGGGCAGTTACCAAGTGC	1080
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1081	ATCCAGGAGTTTGTGGCTGCAAGAAGATCTTTGGGAGCTTGGCATTTCTGCGGAGAG	1140
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
DB	1141	TTTGTATGGGAGCCCAAGCCTCCAAACACTGCCCGCTCCAGCCAGACAGCTCCAAGT	1200
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
DB	1201	GAGACTCTGGAAGAGATCACAGTTTACCTATATACATCTCAGCATGCGCCGACAGCT	1260
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	1261	GACCTCAGCGCTTTCAGAACTTCGAAGTAAATCCGGGAGCAAGTAATCTGCACAA	1320
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1321	TACTCGCTGACCTGCAAGGGCTGGGCATCAGTGGCTGGGGCTGCGCTCACTAGAGGA	1380
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
DB	1381	CTGGCAGTGGACTGGCCCTCATCCACCAACACCCACCTCTGCTTGTGCACACGGTG	1440
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	1441	CCCTGGGACCAAGCTCTTTCGGAACCCGACCAAGCTCTGCTCCACACTGCCAACCG	1500
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	1501	GAGGACAGTGTGTGGGCGAGGGCTGGCTGCCACCAAGCTGTGGCCCGAGGCACTGC	1560
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	1561	TGGGTCCAGGGCCCAACAGTGTGTAACATGCAGCCAGTTCTTTCGGGGCCAGGAGTGC	1620
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
DB	1621	GTGGAGGAATCCGAGTACTCAGGGGCTCCCAAGGAGTATGTGAATGCCAGGCACTGT	1680
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	1681	TTGCGTCCCAACCTTGAGTGTGACCCCAAGATGGCTCAGTGACCTGTGTTTGGACGG	1740
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys	600

Db 1741 GCTGACAGTGTGGGCTGTGCCACTATAAGACCTCCCTTCTGCGTGGCCGCTGC 1800
Qy 601 ProSerGlyVallyProAspLeuSerTyrMetProiletrPlybPheProAspGluGlu 620
Db 1801 CCCAGCGGTGAAACCTGACCTCTCTCATATGCCCATCTGGAATTTCCAGATGAGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCyeThrHisSerCysValAspLeuAspLys 640
Db 1861 GGGCGCATGCCAGCGTTCGCCCATCACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG 1920
Qy 641 GlyCysProAlaGluGlnAlaSerProLeuThrSer----- 653
Db 1921 GGCTGCCCCCGAGCAGAGAGCGCCCTCTGACGTCCATCATCTCTGCGGTGTGGC 1980
Qy 653 ----- 653
Db 1981 ATTCTGCTGCTGCTGCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCGCAG 2040
Qy 653 ----- 653
Db 2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2100
Qy 653 ----- 653
Db 2101 ACACCTAGCGAGCGATGCCCAACAGCGCAGATCGGATCCTTGAAAGAGACGGAGCTG 2160
Qy 653 ----- 653
Db 2161 AGAAGGTGAAGTGTGGATCTGGGCGCTTTGGGCACAGTCTACAAGGCATCTGGATC 2220
Qy 653 ----- 653
Db 2221 CCTGATGGGAGAATGTGAAATTTCCAGTGGCCATCAAAAGTTGTAGGGAAACACATCC 2280
Qy 653 ----- 653
Db 2281 CCCAAAGCCAAAGAAATCTTAGAGAAAGCATACGTGATGCTGTGTGGCTCCCA 2340
Qy 653 ----- 653
Db 2341 TATGTCTCCGCTTCTGGGCACTGCTGCATCCACGGTGAGCTGGTGACACAGCTT 2400
Qy 653 ----- 653
Db 2401 ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCGCGACGCTGGGCTCCAG 2460
Qy 653 ----- 653
Db 2461 GACCTGCTGAATGGTGTATGCAGATTGCCAAGGGGATGAGTACTCTGGAGGATGTGCGG 2520
Qy 653 ----- 653
Db 2521 CTGCTACACAGGACTTGGCGGCTCGGAACGTGCTGAAGAGTCCCAACCATGTCAAA 2580
Qy 653 ----- 653
Db 2581 ATTACAGACTTGGGCTGGCTCGGCTGCTGCAATTGACGACAGAGTACCATGCAGAT 2640
Qy 653 ----- 653
Db 2641 GGGGGCAAGGTGCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTCACC 2700
Qy 653 ----- 653
Db 2701 CACCAGATGATGTGGAGTTATGGTGTACTGTGTGGAGAGTGATGACTTTTGGGGCC 2760
Qy 653 ----- 653
Db 2761 AAACCTTACGATGGATCCCGAGCCCGGAGATCCCTGACCTGCTGGAAAGGGGAGCGG 2820
Qy 653 ----- 653

Db 2821 CTGCCCCAGCCCCCATCTGCAACCATTTGATGTCTCATGATCATGTGTCAAATTTGGATG 2880
Qy 653 ----- 653
Db 2881 ATTGACTCTGAATGTGCGCCCAAGATTCCGGAGCTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGAGCCCCCAGCGCTTTGTGGTTCATCCAGAAATGAGGACTTGGGCCCCAGCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACGACACCTTCTACCGCTCCTGCTGGAGAGCATGACATGGGGACCTTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTTACCCAGCAGGCTTCTTCTGTCCAGACCTTGCCTCCGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3121 GGCATGGTCCACCACAGCAGCCAGCTCATCTACCAGGAGTGGCGTGGGAGCTGCACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGCGCTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCTCCGAAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGGTACCTGGGATGGGGCAGCCAGGGGCTGCAAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCCCACACATGACCCAGCCCTCTACAGCGGTACAGTGAGGACCCACAGTACCCTG 3360
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCCTCTGAGACTGATGGCTACGTGCCCCCTGACCTGACGCCCCAGCCTGAATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCAGCAGATGTTCCGCCCCAGCCCCCTTCCGCCGAGAGGGCCCTCTGCTGCTGCC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGGTGCCACTCTGGAAGGCGCCAGACTCTCTCCCGAGGGAAGATGGGGTC 3540
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGACGTTTTTTCCTTTGGGGGTGGGTGGAGAACCCCGAGTACTTTGACACCCAG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCCCTCAGCCCCCACCCTCTCTCTGCTTCCAGCCAGCCTTCGACCACTC 3660
Qy 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACGAGCCACCCAGAGCGGGGGCTCCACCCAGCAGCTTCAAAGGAGCA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGCGCAGAGAACCCAGAGTACTTGGGTCTGGAGCTGCCAGTG 3765

RESULT 3

US-09-930-125-1
; Sequence 1, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.

APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.544
CURRENT APPLICATION NUMBER: US/09/930.125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3768
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3765)
US-09-930-125-1

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 9 Gaps: 1

US-09-493-480-6 (1-919) x US-09-930-125-1 (1-3768)

QY	1	MetGluLeuAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProGlyAla	20
DB	1	ATGGAGCTGGCGCCTTGTGGCGCTGGGGCTCTCTCGCCCTCTTGGCCCGCGAGCC	60
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
DB	61	GGGAGACCCCAAGTGTGCACCGGCACAGACATGAAGTGGGCTCCTCGCCAGTCCCGAG	120
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
DB	121	ACCCACCTGGACATGCTCCGCCACCTCTACAGGGCTGCGAGTGGTGGTGGAGGAACTG	180
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80
DB	181	GAACCTACCTAGCTGCCCCCAATGCCAGCTGCTCTCTCGAGGATATCCAGAGAGTG	240
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
DB	241	CAGGGCTAGTGTCTATCCTCACAACCAAGTGGGCGAGGTCCACTGGAGGGCTGCG	300
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
DB	301	ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCGCTGACACAATGGA	360
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
DB	361	GACCCGCTGAACAATACCACTGTCACAGGGGCTCCCCAGAGGCTGCGGGAGCTG	420
QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
DB	421	CAGCTTCGAAGCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGGGGAAACCCCG	480
QY	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
DB	481	CTCTGTACAGACACAGATTTTGTGAAGGACATCTTCCACAAGAACCAACAGCTGGCT	540
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	541	CTCACACTATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAG	600
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
DB	601	GGCTCCCGCTGTGGGAGAGAGTCTGAGGATTTGACAGGCTGACGGCGCTGCTGTGT	660
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys	240

DB	661	GCCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGCTGCTGCCACTGAGCAGTGT	720
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	721	GCTGCCGGTGCACGGGCCCAAGCACTCTGACTGCTGGCTGCTCCTCCTCAACCCAC	780
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
DB	781	AGTGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTACACACAGACAGCTTTGAG	840
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
DB	841	TCCATGCCCAATCCCGAGGGCCGTATACATTCGGCGCCAGCTGTGTGACTGCTGCTCC	900
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	901	TACAACTACCTTTCTACGGACGTGGATCCTGCACCTCTGCTGCCCTGTCACACCA	960
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
DB	961	GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAGTGGCAGCAAGCCCTGTGCC	1020
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1021	GTGTCTATGTGCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACCACTGCAAT	1080
QY	361	IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1081	ATCCAGGAGTGTGCTGGCTGCAAGAGATCTTTGGAGCTGGCATTTCTGCCGAGAGC	1140
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe	400
DB	1141	TTTGATGGGACCCAGCCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1200
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
DB	1201	CAGACTCTGGAAGAGATCACAGTTTACCTATATACATCTCAGCATGCGCGGACAGCT	1260
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	1261	GACCTCAGCGTCTTCAGAACCTGCAAGTAATCCGGGACAGAAATCTGCACAATGGCG	1320
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1321	TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGTGGGCTGCGCTCACTGAGGAA	1380
QY	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480
DB	1381	CTGGCAGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTGTGCACACGGTG	1440
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	1441	CCCTGGGACCACTCTTTCCGAAACCCGACCAAGCTTGTCTCCACTGCCAACCGGCCA	1500
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	1501	GAGGACAGTGTGTGGCGAGGGCTGGCTGCCACACAGCTGTGCGCCCGGCGCACTGC	1560
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	1561	TGGGTCCAGGGCCCAACCCAGTGTCACTGACAGCTGCTGCTTCTGGGGCGAGGATGC	1620
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
DB	1621	GTGGAGGAATCCGAGTACTGCGGGGCTTCCCGAGGAGTATGTGATGCCAGGCACTGT	1680
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	1681	TTGCCGTGCCACCTGTAGTGTGAGCCCAAGATGCTCAGTGCCTGTTTGGACCGGAG	1740
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
DB	1741	GCTGACCAAGTGTGGCGCTGTGCCCACTATAAGGACCTCTCCCTTGTGGTGGCCGCTGC	1800

Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
Db	1801	CCCAGCGGTGTGAACCTGCACCTCTCTCTACATGCCCATCTGGAAGTTTCAGATGAGGAG	1860
Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
Db	1861	GGCGATGCCAGCCTTGCCCCATCAACTGCACCCACCTCCTGTGTGGACCTGGGATGACAAG	1920
Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	1921	GGCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGTACGTTCCATCTCTCGCGGTGTTGGC	1980
Qy	653	-----	653
Db	1981	ATTCTGCTGTTGTTGTTGGGGTGGTCTTTTGGGATCCTCATCAAGCAGCAGCAGCAG	2040
Qy	653	-----	653
Db	2041	AAGATCCGGAAGTACACGATCGGAGACTGCTGCAGGAAACGGAGCTGTGGAGCCGCTG	2100
Qy	653	-----	653
Db	2101	ACACTAGCGGAGCGATGCCCAACCGCGCAGATCGGATCTCTGAAGAGACGGAGCTG	2160
Qy	653	-----	653
Db	2161	AGGAAGGTGAAGTGCTTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGCGCATCTGGATC	2220
Qy	653	-----	653
Db	2221	CCTGATGGGAGAAATGTGAAMATTCAGTGGCCATCAAAGTGTGTGAGGGAACACATCC	2280
Qy	653	-----	653
Db	2281	CCCAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGGTCTCCCA	2340
Qy	653	-----	653
Db	2341	TATGTCTCCGCGCTTCTGGGCATCTGCCTGCATCCACGCTGCAGCTGTGCACACAGCTT	2400
Qy	653	-----	653
Db	2401	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAACCGCGGACGCCCTGGGCTCCAG	2460
Qy	653	-----	653
Db	2461	GACCTCTGMACTGGTGTATGCAGATTGCCAAGGGATGAGTACCTGGAGGATGTGCGG	2520
Qy	653	-----	653
Db	2521	CTCGTACACAGGGAATTGGCGCGCTCGGAACGTGTGTTCAAGAGTCCCAACCATGTCAAA	2580
Qy	653	-----	653
Db	2581	ATTACAGACTTCGGGCTGGCTCGCTGTCAGACATTGACGAGACAGAGTACCATGCAGAT	2640
Qy	653	-----	653
Db	2641	GGGGCAAGTGCACCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGCGGTTCAACC	2700
Qy	653	-----	653
Db	2701	CACCAGAGTANGTGTGGAGTTATGGTGTGACTGTGTGGAGTGTATCTTTTGGGGCC	2760
Qy	653	-----	653
Db	2761	AAACCTTACGATGGATCCACGCCGCGGAGATCCCTGACCTGCTGGGAAAGGGGAGCGG	2820
Qy	653	-----	653
Db	2821	CTGCCCAGCCCCCATCTGCACCATTTGATGTTCTACATGATCATGTGTCAAAATGTTGGATG	2880

Qy	653	-----	655
Db	2881	ATTGACTCTGAATGTTCGGCCCAAGATTCCGGGAGTTGTGTGAATTCTCCCGCATGCC	2940
Qy	654	-----	656
Db	2841	AGGACCCCGCAGCGCTTTGTGGTTCATCCGAATGAGGACTTGGGCCGAGCGATCCCTTG	3000
Qy	665	AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	3001	GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT	3060
Qy	685	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	704
Db	3061	GAGGAGTATCTGGTACCCAGCAGGCGTCTTCTGTCCAGACCTGCGCCGGCGCTGGG	3120
Qy	705	GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr	724
Db	3121	GGCATGTGTCCACACAGGACCGGAGCTCATCTACAGGAGTGGCGTGGGACCTGACA	3180
Qy	725	LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly	744
Db	3181	CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCACAGGTCTCCATGGGACCTCCGAAGG	3240
Qy	745	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer	764
Db	3241	GCTGGCTCCGATGTATTGTATGTGTGACTTGGGAATGGGGGAGCCAAAGGGCTGCAAGC	3300
Qy	765	LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu	784
Db	3301	CTCCCCACATGACCCACGCCCTCTACAGCGGTACAGTGGAGACCCCAAGTACCCCTG	3360
Qy	785	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal	804
Db	3361	CCCTCTGAGACTGATGGCTAGTTGGCCCCCTGACCTGAGCCCCCAGCTGGAATATGTG	3420
Qy	805	AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla	824
Db	3421	AACGAGCCAGATGTTGGGCCCCAGCCCTTCGCCGAGAGGGGCCCTCTGCTGCTGCC	3480
Qy	825	ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal	844
Db	3481	CGACCTGCTGGTGCCACTCTGGAAGAGCCCAAGACTCTCTCCCCAGGAGAAATGGGGTC	3540
Qy	845	ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln	864
Db	3541	GTCMAAGACGTTTTTGGCTTTGGGGTGGCGTGGAGAACCCCGAGTACTTGCACACCCAG	3600
Qy	865	GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu	884
Db	3601	GGAGGAGCTGCCCTCAGCCCCACCCCTCTCTCTGCTTTCAGCCAGGCTTCGACAACCTC	3660
Qy	885	TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr	904
Db	3661	TATTACTGGGACGAGGACCCACGAGCGGGGGCTCCACCCAGCACTTCAAAGGGACA	3720
Qy	905	ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal	919
Db	3721	CCTAGGCGAGAGAACCCAGAGTACTGGGTCTGGACGTGCCAGTG	3765
RESULT 4			
US-10-313-644-1			
; Sequence 1. Application US/10313644			
; Publication No. US20030157119A1			
; GENERAL INFORMATION:			
; APPLICANT: Gaiger, Alexander			
; APPLICANT: Cheever, Martin A.			
; APPLICANT: Hand-Zimmerman, Susan			
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL			
; TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES			
; FILE REFERENCE: 210121.483C3			
; CURRENT APPLICATION NUMBER: US/10/313,644			
; CURRENT FILING DATE: 2002-12-04			


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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-313-644-1

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservatives: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 336 Indels: 336
DB: 16 Gaps: 1

US-09-493-480-6 (1-919) x US-10-313-644-1 (1-3768)

QY 1 MetGluLeuAlaLeuAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProGlyAla 20
DB 1 ATGGAGCTGGCGGCTTGTGGCGCTGGGGCTCTCTCGCCCTCTTGGCCCGCGAGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 61 GCGAGCACCAGTGTGCACCGGCACAGACATGAAAGTGGCTCTCTGCCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 121 ACCCACCCTGGACATGTCTCGCCACCTCTACCAAGGCTGCGAGTGGTGGTGGAGAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
DB 181 GAACTCACCTAGCTGCTCCACCAATGCCAGCTGTCTCTCGAGGATATCCAGAGGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 241 CAGGGCTAGTGTCTATCTGCTCACAACCAAGTGGAGGAGTCCCTCCAGAGGTGGCG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
DB 301 ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCGCTGTAGACAAATGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 361 GACCCGCTGAACAATACCACTGTCACAGGGGCTCCCAAGGAGGCTGCGGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 421 CAGCTTCGAGGCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCAAG 480
QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
DB 481 CTCTGTACAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTTGCCACCTGTCTCCGATGTGTAAAG 600
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 601 GGCCTCCGCTGTGGGAGAGAGATTCTGAGGATTGTTCAGAGCTGACCGGCACCTGTCTGT 660
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
DB 661 GCCGGTGGCTGTGCCGCTGCAAGGGCCCACTGCCCACTGCTGCTGCTGCTGCTGCTGCTG 720
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 721 GCTGCCGCTGCACGGGCCCCAAGCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

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261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
781 AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTACAAACACACACACGCTTTGAG 840
281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
841 TCCATGCCCAATCCCGAGGGCGGTATACATTTCCGGCGCAGCTGTGTGACTGCCTGTGCC 900
301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
901 TACAACTACCTTTCTACGGACGTGGGATCTGCACCCCTGCTGCCCTGTCACAAACCAA 960
321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
961 GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCCGA 1020
341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
1021 GTGTCTATGTGTCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTTACCAGTGCCTAT 1080
361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
1081 ATCCAGGAGTTTGTCTGGCTGCAAGAGATCTTTGGAGGCTTGGCATTTCTGCCGAGAGC 1140
381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
1141 TTTGATGGGACCCAGCCCTCCAAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1200
401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
1201 GAGACTCTGGAGAGATCACAGGTTACCTATATACATCTCAGCATGCGCGGACAGCTGCCT 1260
421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
1261 GACCTCAGCGTCTTCAGAACCTGCAGTAATCCGGGAGCAGTAATCTGCACAAATGGCGCC 1320
441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
1321 TACTCGCTGACCTGCAAGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCACTCAGAGGAA 1380
461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
1381 CTGGCAGTGGACTGGCCCTCATCCACCAATAACACCCACCTCTGCTTGTGTGCACAGGTG 1440
481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
1441 CCCTGGGACCACTCTTTCGGNACCCGACCAAGCTTGTCTCCACACTGCCAAACCGGCCA 1500
501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
1501 GAGGACGAGTGTGGCGAGGGCTGGCTGCCACCACTGCTGCCCGCGAGGCACTGC 1560
521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
1561 TGGGTTCAGGGGCCACCCAGTGTGTCAACTGCAGCAGTTCCTTCGGGGCCAGGAGTGC 1620
541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
1621 GTGGAGGAATCCGAGTACTGCGGGGCTCCCGCAGGAGTATGTGNAATGCCAGGCACTGT 1680
561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
1681 TTGCCGTGCCACCTGAGTGTGAGCCCGCAGAAATGGCTCAGTGCCTGTTTGGACCGGAG 1740
581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
1741 GCTGACCACTGTGGCTGTGCCCTGTCACATAAGGACCCCTCCCTTCTGCGGTGGCCCTGC 1800
601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
1801 CCCAGCGGTGGAACCTGACCTCTCTACATGCCCATCTCGAAGTTTCCAGATGAGGAG 1860
621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640

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1861 GGCATGCGCAGCCTTCCCATCACTGACCCACCTCTGTGTGGACCTGGATGACAAG 1920
641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
1921 GGCTGCCCCCGCAGCAGAGCCAGCCCTCTGACGTCCATCATCTCTGCGGTGGTGGC 1980
653 653
1981 ATTTCTGCTGTCGTGTGTTTGGGGTGTGTTTGGGATCCTCATCAAGCGACGCGCAGCAG 2040
653 653
2041 AAGATCCGGAAGTACAGATGCGGAGACTCTGTCAGGAAACGGAGCTGTGTGGAGCCGCTG 2100
653 653
2101 ACACCTAGCGGAGGATGCCAACACGCGCAGATCGGATCCTGAAAGAGACGGAGCTG 2160
653 653
2161 AGGAAGTGAAGTGTCTTGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220
653 653
2221 CCTGATGGGGAGAAATGTGAAAATTCAGTGGCCATCAAGTGTGAGGGAACACATCC 2280
653 653
2281 CCCAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGCTGTGTGGGCTCCCCA 2340
653 653
2341 TATGTCTCCCGCTTCTGGGCATCTGCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2400
653 653
2401 ATGCCCTATGGTCTCTTAGACCATGTCCGGGAAACCGCGAGCCCTGGGCTCCAG 2460
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653 653
2641 GGGGGCAAGTGGCCCATCAAGTGGATGGCCCTGGAGTCCATTCTCCGCGCGGTTCAAC 2700
653 653
2701 CACCAGAGTGTGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
653 653
2761 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTGTGAAAGGGGGAGCGG 2820
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2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAATGTTGGATG 2880
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2881 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
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2941 AGGGACCCCCAGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGGCCCCAGCGTCCCTTG 3000
665 AspSerThrPheTyrArgSerLeuLeuAspAspMetGlyAspLeuValAspAla 684
3001 GACAGCACCTTCTACCGCTCACCTGTGGAGACGATGACATGGGGACCTGGTGTGATGCT 3060
685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
3061 GAGGAGTATCTGTGTACCCAGCAGGCGCTTCTTGTGTCCAGACCTTGCCTCCGGCGCTGGG 3120
705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
3121 GGATGGTCCACCACAGCACCGCAGCTCATCTACAGGAGTGGCGGTGGGACCTGCACA 3180
725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCAGGTCTCCACTGGCACCTCCGAAGGG 3240
745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyGlyLeuGlnSer 764
3241 GCTGGCTCCGATGATATTGATGTGACCTGGGAATGGGGCAGCCAAAGGCTGCAAGC 3300
765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
3301 CCCCCACACATGACCCCGCCCTCTACAGCGGTACAGTCAAGACCCCAAGTACCCCTG 3360
785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
3361 CCTCTGAGACTGATGGCTAGCTTGGCCCCCTGACCTGACAGCCCCCAGCCTGAATATGTG 3420
805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
3421 AACCCAGCAGATTTGGGCGCCAGCCCTTCCGCCCGAGAGGGCCCTCTGCTCTGCTGCC 3480
825 ArgProAlaGlyAlaThrLeuGluArgProLeuThrLeuSerProGlyLysAsnGlyVal 844
3481 CGACCTGCTGGTGGCCACTCTGGAAGGCCCCAGACTCTCTCCCGAGGAGAAATGGGGTC 3540
845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
3541 GTCANAGAGCTTTTGGCTTGGGGTGGCGTGGAGAACCCCGAGTACTTTGACACCCAG 3600
865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 884
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RESULT 5

US-09-441-411-5
; Sequence 5, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-441-411-5

Alignment Scores:

Pred. No.: 0 Length: 4473
 Score: 4900.00 Matches: 919
 Percent Similarity: 73.23% Conservative: 0
 Best Local Similarity: 73.23% Mismatches: 0
 Query Match: 96.49% Indels: 336
 DB: 10 Gaps: 1

US-09-493-480-6 (1-919) x US-09-441-411-5 (1-4473)

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 QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 DB 235 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTCGCGCTCCCTGCCAGTCCCGAG 294
 QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnValAsnLeu 60
 DB 295 ACCACCTGGACATGCTCCGCCACCTCTACCAAGGCTGCAGGTGTGCGAGGAACCTG 354
 QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
 DB 355 GAACTCACCTACTGCCCCACCAATGCCAGCCTGTCTCTCTCGAGGATATCCAGAGGTG 414
 QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
 DB 415 CAGGGCTAGCTGTCTCATCTGCACCAAGTGAGCGAGGTCCCACTGCAGAGGTGCGG 474
 QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
 DB 475 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTGTACAAATGA 534
 QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 DB 535 GACCCGCTGAACAATACCAACCCCTGTTCACAGGGGCTCCCGAGGCGCTCGGGAGCTG 594
 QY 141 GlnLeuArgSerLeuThrGlnIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
 DB 595 CAGCTTCGAAGCCTCACAGAGATCTTGAAGAGGGGTCTTGTATCAGCGGAACCCCGAG 654
 QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla 180
 DB 655 CTCCTGTACAGGACACGATTTTGTGGAAGGACATCTTCCACAGAACACACAGCTGGCT 714
 QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
 DB 715 CTCACACTGATAGACACCAACCGCTCTCGGGCTTGCACCCCTGTCTCCGATGTGAAG 774
 QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
 DB 775 GGCTCCCGCTGTCTGGGAGAGATTTGTGAGGATTTGTTCAGAGCCTGACCGCACCTGTCTGT 834
 QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
 DB 835 GCCGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCCACTGCTGTCTGCCATGAGCAGTGT 894
 QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 DB 895 GCTGCCGGCTGCAGCGGGCCCCAAGCACTCTGACTGCTGCGCTGCGCTCCCTCCACITCAACCCAC 954
 QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
 DB 955 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTACACACAGACACGCTTTTGAG 1014
 QY 281 SerMetProAsnProGluGluValArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
 DB 1015 TCATGTCCCAATCCCGAGGGCGGTATATATTGCGGCCCGCAGCTGTGTGACTGCTGCTGCC 1074
 QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320

DB 1075 TACAACTACCTTCTACGAGCGTGGGATCCTGCACCCCTCGTCTGCCCTCGCACCAACCA 1134
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 DB 1195 GTGTCTATGTCTGGGCATGGAGGACCTTGCAGAGGTGAGGGCAGTTACCACTGCCCAAT 1254
 QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
 DB 1255 ATCCAGGAGTGTCTGGCTGCAGAAGATCTTTGGAGGCTTGGCATTTCTGCGGAGAGC 1314
 QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
 DB 1315 TTTGATGGGGACCCAGCCTCCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1374
 QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
 DB 1375 GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGCGCGGACAGCTGCCT 1434
 QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisGlnGlyAla 440
 DB 1435 GACCTCAGCGCTTCTCCAGAACCTGCAGATTAATCCGGGACGAATCTGCACAATGGCGC 1494
 QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
 DB 1495 TACTCGCTGACCCCTCAAGGGCTGGGCATCAGCTGGCTGGGGCTCGCTCCTCAGTGGGAA 1554
 QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
 DB 1555 CTGGGCGAGTGGACTGGCCCTCATCCACCAATACACCCACTCTCTGTTGTTGACACGGTG 1614
 QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
 DB 1615 CCCTGGGACCAAGCTCTTTCGGAACCCGACCAAGCTCTGCTCCACTGCCAACCGGCCA 1674
 QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
 DB 1675 GAGGACAGTGTGTGGGCGAGGGCTGGCCCTGCCACAGCTGTGCGCCCGGAGGCACTGC 1734
 QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
 DB 1735 TGGGTTCCAGGGCCACCCAGTGTCTCACTGCAGCCAGTCTCTTTCGGGGCCAGGAGTGC 1794
 QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
 DB 1795 GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1854
 QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
 DB 1855 TTGCCGTGCCACCTTGAGTGTGAGCCCGCAGAAATGGCTCAGTGACTGTGTTTGGACCGGAG 1914
 QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
 DB 1915 GCTGACCAAGTGTGGCTGTGCCCACTATAAGGACCTTCCCTTCTGCGTGGCCGCTGC 1974
 QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
 DB 1975 CCCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTCAGATGAGGAG 2034
 QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAsnLeuAspLys 640
 DB 2035 GCGCATGCCAGCTTGGCCCATCAACTGACCCCACTCTCTGTGTGAGACCTGATGACAAG 2094
 QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
 DB 2095 GGCTGCCCGCGGACGAGAGAGCCCTCTGACGTCCATCATCTCTCGGGTGGTTGGC 2154
 QY 653 ----- 653

Db 2155 ATTCTGCTGGTCTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2214
Qy 653 ----- 653
Db 2215 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAACGGAGCTGGTGGAGCCGCTG 2274
Qy 653 ----- 653
Db 2275 ACACCTAGCGAGCGATGCCCAACAGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2334
Qy 653 ----- 653
Db 2335 AGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACTGTACAAAGGGCATCTGGATC 2394
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Db 2455 CCCAAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGGTCCCCCA 2514
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Db 2695 CTGCTACAGGACTTTGGCGCTCGGAACGTGCTGAAGTCCCAACCATGTCAAA 2754
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Db 2755 ATTACAGACTTCGGGCTGGCTCGGCTGCTGACATTGACGACAGAGTACCATGCAGAT 2814
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Db 3055 ATTGACTCTGAATGTGGGCCAAGATTCGGGAGTGGTGTCTGAAATTTCTCCCGCATGGCC 3114
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGGACCCCGCGCTTTGGTTCATCCAGAAATGAGGACTTGGGCCAGCCAGTCCCTTG 3174
Qy 665 AppSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAla 684
Db 3175 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT 3234
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3295 GGCATGGTCCACCACAGGCACCGCAGCTCATCTACAGGAGTGGCGGTGGGACCTGCACA 3354
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCGCCAGGTCTCCACTGGCACCTCCGAAGGG 3414
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3415 CTTGGCTCCGATGATTTGATGGTGACCTGGGAAATGGGGCAGCCAGGGGCTGCAAGC 3474
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3475 CTCCCCACACATGACCCCGCTCTACAGCGGTACAGTGAGGACCCACAGTACCCCTG 3534
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCTCTGAGACTGATGGCTACGTTGCCCCCTGACCTGCAGCCCCCAGCTGAATATGTG 3594
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACACCCAGATGTTTGGCCCCAGCCCCCTTCCGCCCGAGAGGGCCCTCTGCCTGCTGCC 3654
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGCTGGTGCCACTCTTGGAAAGGCCCAAGACTCTCTCCCGCAGGAAAGATGGGGTC 3714
Qy 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAGAGAGCTTTTTCCTTGGGGGTGGCGTGGAGAACCCCGAGTACTTGGACACCCAG 3774
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GAGGAGCTGCCCCCTCAGCCCCACCTCTCTGCTGCTTACGCCAGGCTTCGACCAACTC 3834
Qy 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGGACCCAGGACCCACAGAGCGGGGGCTCCACCCAGCACCTTCAAAGGGACA 3894
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGGCAGAGAACCAGAGTACCTGGGTCTGGACGTGCCAGTG 3939

RESULT 6
US-10-146-473-32
; Sequence 32, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; FILE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-473-32

Alignment Scores: 0 Length: 4473
Pred. No.: 4900.00 Matches: 919
Score:

Percent Similarity: 73.23%	Conservative: 0
Best Local Similarity: 73.23%	Mismatches: 0
Query Match: 96.49%	Indels: 336
DB: 15	Gaps: 1
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Db 175 ATGGAGCTGGCGGCTTGTGGCGCTGGGGCTCCTCGCCCTCTTGGCCCCCGGAGCC 234	Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40	Db 1195 GTGTCTATGGTCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACCAAGTGCCAAAT 1254
Db 235 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGAGCTCGGCTCCCTGCCAGTCCCGAG 294	Qy 361 IleGlnGluPheAlaGlyCysGlyLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60	Db 1255 ATCCAGGAGTTTGTCTGGCTGCAAGAAGATCTTTGGAGCGCTGGCATTTCTGCCGAGAGC 1314
Db 295 ACCACCTGACATGCTCGGCACCTCTACCAAGGCTGCCAGGTGGTGACAGGAACCTG 354	Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80	Db 1315 TTTGATGGGAGCCCAAGCCTCAACACATGCCCGCTCCAGCGAGCAGCTCCAAGTGTGT 1374
Db 355 GAACCTCACCTACCTGCCACCAATGCCAGCTGTCTTCTTCCAGGATATCCAGAGGTG 414	Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTspProAspSerLeuPro 420
Qy 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100	Db 1375 GAGACTCTGGAAAGAGATCACAGGTACCTATACATCTCAGCATGGCCGCGACAGCTGCCT 1434
Db 415 CAGGGCTAGCTGCTCATCGCTCACAAACCAAGTGAAGCGAGGTCCCACTGCAGAGCTCGG 474	Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120	Db 1435 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGAGCGAATTTCTGCACAAATGGGCG 1494
Db 475 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCGGTGCTAGACAATGGA 534	Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140	Db 1495 TACTCGCTGACCTGCACAGGCTGGGCATCAGCTGGCTGGGGCTGCCTCCTCATGTAGGGAA 1554
Db 535 GACCCGCTGAACATAACACCCCTGTACAGGGGCTTCCCAGGAGGCTCGGGAGCTG 594	Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Qy 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuLeuGlnArgAsnProGln 160	Db 1555 CTGGGAGTGAAGTGGCCCTCATCCACCATTAACCCACCTCTCTGCTTGTGTGCACACGGTG 1614
Db 595 CAGCTTCGAAGCCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAAACCCCGAG 654	Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla 180	Db 1615 CCCTGGGACCAAGCTCTTTTCGGAAACCCGACCAAGCTCTGTCTCCACACTGTCACACCGGCCA 1674
Db 655 CTCTGTACAGAGACAGATTTTGTGGAAGGACATCTTCCACAAAGAACCAACAGCTGGCT 714	Qy 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200	Db 1675 GAGGACAGAGTGTGTGGCGAGGGCTGGCTGCCACCAAGCTGTGGCGCCGAGGGCACTGC 1734
Db 715 CTCACACTGATACACACCAACCGCTCTCGGGCTTCCACCCCTGTCTCCGATGTGTAA 774	Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Qy 201 GlySerArgCysTrpGlyGluSerGluAspCysGlnSerLeuThrArgThrValCys 220	Db 1735 TGGGTCCAGGCCCCACCCAGTGTCACTGACAGCCAGTTCTCTTCGGGCCACAGAGTGC 1794
Db 775 GGCTCCCGCTGTGGGAGAGAGTTCTGAGGATTTGTACAGCGCTGACGCGCACTGTCTGT 834	Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240	Db 1795 GTGGAGGAATCCGAGTACTGCAGGGGTCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1854
Db 835 GCGGGTGGCTGTGCCCGCTGCAAGGGGGCACTGCCCACTGACTGCTGCATGACAGCAGTGT 894	Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260	Db 1855 TTGCGCTGCCACCTCTGAGTGTGAGCCCGAGAAATGGCTCAGTGAACCTGTTTTGGACCGGAG 1914
Db 895 GCTTGGCGCTGCACGGGCCCCAAGGCACTCTGACTGCTGGCTGGCTCCCTTCCATTCACAC 954	Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaAtqCys 600
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280	Db 1915 GCTGACCAAGTGTGGCTGTGCCACATATAAGGACCCCTCCCTCTCGGTGGGCCCGCTGC 1974
Db 955 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTCAACACAGACACAGTCTTGGAG 1014	Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300	Db 1975 CCCAGCGGTGTGAACCTGACCTCTCCTACATGCCCCATCTGGAAGTTTCCAGATGAGGAG 2034
Db 1015 TCCATGCCCAATCCCGAGGGCGGTATACATTCGCGCGCAGCTGTGTGACTGTCCTGTCCC 1074	Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320	Db 2035 GCGCATGCCAGCTTGGCCCATCAACTGCACCCCACTCCTGTGTGGACCTGGATGACAAG 2094
Db 1075 TACAACTACTTTCTACGACAGGTGGATCCTGCACCCCTCGTCTGGCTGGCTGTGACTGTC 1134	Qy 641 GlyCysProAlaGluGlnArgAsnProLeuThrSer 663
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340	Db 2095 GGCTGCCCGCGAGCAGAGCAGCCCTCTGACGTCCCATCATCTCTGCGGTGGTTGGC 2154
	Qy 653 ----- 653
	Db 2155 ATTCTGCTGGTGGTCTTGGGGTGGTCTTTGGGATCTCTCATCAAGCGACGCGACGAG 2214
	Qy 653 ----- 653
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QY 653 ----- 653
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QY 653 ----- 653
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QY 653 ----- 653
Db 3055 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCCGATGGCC 3114
QY 654 -----GlnAsnGluAspLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3115 AGGGACCCCGCGCTTTGTGTCTATCCAGAAATGAGACTTTGGGCCCGACGCTCCCTTG 3174
QY 665 AppSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGTGTGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTATACCCACGAGGGCTTCTTCTGTCCAGACCTTGCCTGGCGCGCTGGG 3294
QY 705 GlyMetValHisIleArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3295 GGCAATGTCACACAGGACCCAGCTCATCTACCAGGAGTGGCGGTGGGACCTTGACA 3354
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QY 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGCGCTGGAGCCCTCTGAAGAGGAGGCGCCCGCAGGTCTCCACTGGCACCTCCGAAGG 3414
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyLeuGlnSer 764
Db 3415 GCTGGCTTCGATGTATTTGATGTGACCTGGGAAATGGGGCAGCCCAAGGGGCTGCAANGC 3474
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3475 CTCCCCACACATGACCCCGCCCTCTACAGCGGTACAGTGAGGACCCACAGTACCCCTG 3534
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCTCTGAGACTGATGGCTACGTTGCCCGCTGACCTGCAGCCCCCAGCCCTGAATATGTG 3594
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACCCAGCCAGATGTTCCGGCCCCCAGCCCTTTCGCCCGGAGAGGCGCTCTGCTCTGCTGCC 3654
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGCTGGTGCCTACTCTGGAAAGGCCCAAGACTCTCTCCCCAGGGAAGATGGGGTC 3714
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
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QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGCTGCCCTCAGCCCCCAGCCCTCTCTCTGCTTTCAGCCAGCCTTCGACCAACCTC 3834
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGGACGAGCCACCAGAGCGGGGGCTCCACCCAGCACCTTTCAGCAAGGACA 3894
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Db 3895 CCTACGCGACAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3939

RESULT 7
US-10-207-655-44
; Sequence 44, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-207-655-44

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 15 Gaps: 1

US-09-493-480-6 (1-919) x US-10-207-655-44 (1-4473)

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Db 175 ATGGAGCTGGCGGCTTTGTGCGCTGGGGCTCTCTCTGCGCTCTTGGCCCCCGGAGCC 234
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DB	235	GGGAGACCAAGTGTGACCCGGCAGACATGAGTGGGCTCCTCCAGTCCCGAG	294				
QY	41	ThrHisLeuAspMetLeuArgHisLeuThrGlnGlyCysGlnValValGlnGlnArgLeu	60		401	GluThrLeuGluGluIleThrGlyThrLeuThrIleSerAlaThrProAspSerLeuPro	420
DB	295	ACCCACTGGACATGTCGCCCACTCTACCAAGGCTGCCAGGCTGCCAGTGGTGGAGAACCTG	354		1375	GAGACTCTGGAGAGATCACAGTTACCTATACATCTTCAGCATGGCCGACAGCTGCCT	1434
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80		421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	355	GAACCTACACTGCTGCCCAACCAATGCCAGCTGTCTCTCCAGGATATCCAGAGGTG	414		1435	GACCTCAGGCTTCCAGAACCTGCAGTAATCCGGGACGAATCTGCACAAATGGCGCC	1494
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100		441	TyrSerLeuThrLeuGlnGlnGlyLeuGlyIleSerThrLeuGlyLeuArgSerLeuArgGlu	460
DB	415	CAGGGCTACGTCTCATCTCTCAACCAAGTGGGACAGTCCCACTGCAGAGGCTGCGG	474		1495	TACTCGTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCCTCACTAGGGAA	1554
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120		461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
DB	475	ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGACAAATGA	534		1555	CTGGGACGTGGACTGGCCCTCATCCACCATAAACCCACCTCTGCTTCGTGCACACGGTG	1614
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140		481	ProThrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	535	GACCCGCTGAACAATACACCCCTGTCAAGGGGCTCCCGAGGAGGCTGGCGGAGCTG	594		1615	CCCTGGGACCAGCTCTTTCGGAAACCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1674
QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160		501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	595	CAGCTTCGAAGCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCA	654		1675	GAGGACGAGTGTGGCGAGGGCTGGCTGCCACCACTGTGGCCCGAGGGCACTGC	1734
QY	161	LeuCysTyrGlnAspThrIleLeuThrLysAspIlePheHisIleLysAsnGlnLeuAla	180		521	ThrGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	655	CTCTGTACAGGACACGATTTTGTGGAAGGACATCTTCACAAAGAACCAACAGCTGGCT	714		1735	TGGGTCCAGGGCCACCCAGTGTCTCACTGCAGCCAGTTCTCTTCGGGGCCAGGATGC	1794
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200		541	ValGluGluCysArgValLeuGlnGlyLeuProArgGlyTyrValAsnAlaArgHisCys	560
DB	715	CTCACACTGATAGACACCAACCGCTCTCGGGGCTGCCACCCCTGTCTCCGATGTGAAG	774		1795	GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCGACGGAGTATGTGAATGCCAGGCACTGT	1854
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220		561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	775	GGCTCCCGTGTGGGAGAGAGTTCTGAGGATTTGTACAGGCTTGACGGCGCACTGTCTGT	834		1855	TTGCGGTGCCACCTGAGTGTGAGCCAGAGATGCTCAGTCAGCTGTTTGGACCGGAG	1914
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240		581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
DB	835	GCCGCTGGTGTGCCCGCTGCAAGGGCCACTGCCCACTGCTGCTGCCATGAGCAGTGT	894		1915	GCTGACCACTGTGGCTGTGCCCACTATAAGGACCTCTCTCTGCGTGGCCCGCTGC	1974
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260		601	ProSerGlyValLysProAspLeuSerTyrMetProIleThrLysPheProAspGluGlu	620
DB	895	GCTGCCGCTGCACGGGCCCAAGCACTCTGACTGCTGGCTGCCCTCCACATTCACACAC	954		1975	CCGACGGTGTGAACCTGACCTCTCTACATGCCCACTCTGGAAGTTTCCAGATGAGGAG	2034
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280		621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
DB	955	AGTGGCATCTGTGAGCTGCCCTGCCAGCCCTGGTCACCTACACACACACACACGTTTGAG	1014		2035	GGCGCATGCCAGCTTGCCCATCAACTCACTGACCCCACTCTCTGTGTGGACCTGGATGACAAG	2094
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300		641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer-	653
DB	1015	TCCATGCCCAATCCCGAGGCGCGGTATACATTCGGCGCCAGCTGTGTGACTGCCTGTCCC	1074		2095	GGCTCCCCCGCGAGCAGAGAGCCCTCTGACGTCCATCATCTCTCGGTGGTGTGC	2154
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320		653	-----	653
DB	1075	TACAACTACTCTTCTACGAGCGTGGATCTCTGACCCCTCGTCTGCCCTCCCTGCACAAACAA	1134		2155	ATTCTGCTGCTGCTGGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCAGCGGACAGCAG	2214
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340		653	-----	653
DB	1135	GAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCGA	1194		2215	AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGAGCTGTGTGGAGCCGCTG	2274
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360		653	-----	653
DB	1195	GTGTGCTATGTGTGGGCATGGAGCACTTGCAGAGGTGAGGCGAGTTTACCAGTGGCCAA	1254		2275	ACACCTAGCGGAGCGATGCCCAACCGCGCGCAGATGCGGATCCTCTGAAGAGAGCGGAGCTG	2334
QY	361	IleGlnGluPheAlaGlyCysValLysIlePheGlySerLeuAlaPheLeuProGluSer	380		653	-----	653
DB	1255	ATCCAGAGTGTGCTGGCTGGCAAGAGATCTTTGGGAGGCTGGCATTTCTGCGGAGAG	1314		2335	AGGAAGGTGAAGTGTCTTGGATCTGGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC	2394
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400		653	-----	653


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Db 2395 CTTGATGGGGAGAAATGTGAAAAATTCAGTGGCCCATCAAGTGTGAGGGAAAAACACATCC 2454
QY 653 -----
Db 2455 CCCAAAGCCAAACAAAGAAATCTTAGAGAGACATACGTGATGGTGTGGGCTCCCCA 2514
QY 653 -----
Db 2515 TATGTCTCCGCGCTTCTGGGCATCTGCTGACATCCACGGTGACGCTGTGTGACACAGCTT 2574
QY 653 -----
Db 2575 ATGCCCTATGGCTGCCCTTTAGACCATGTCCGGGAAAAACCGCGGACGCGCTGGGCTCCAG 2634
QY 653 -----
Db 2635 GACCTGTGTAAGTGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTCCGG 2694
QY 653 -----
Db 2695 CTCGTACACAGGACTTGGCGCTCGGAACGTGCTGTCAAGAGTCCCAACCATGTCAAA 2754
QY 653 -----
Db 2755 ATTACAGACTTCGGGTGGCTCGGCTGTGTGCAATTGACAGACAGATACCATGCGAGAT 2814
QY 653 -----
Db 2815 GGGGGCAAGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTCAAC 2874
QY 653 -----
Db 2875 CACCAGAGTATGTGTGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934
QY 653 -----
Db 2935 AAACCTTACATGGGATCCAGCGCGGAGATCCCTGACCTGTGGAAGGGGGAGCGG 2994
QY 653 -----
Db 2995 CTGCCCGAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGGTCAAAATGTTGGATG 3054
QY 653 -----
Db 3055 ATTGACTCTGAATGTCCGCCAAGATTCCGGGAGTTGGTGTCTCAATTTCTCCGCATGGCC 3114
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGGACCCCGAGCGCTTTGTGGTCAATCCAGAAATGAGGACTTGGGCCCGAGCAGTCCCTTG 3174
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGACCTTTCTACCGCTCACTGCTGGAGACGATGACATGGGGACCTGGTGGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTACCCAGCAGGGGCTTCTTCTGTCCAGACCTGCCCCGGCGCTGGG 3294
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3295 GGATGGTCCACACAGGACCCAGCTCATCTACAGGAGTGGCGGTGGGGACCTGCACA 3354
QY 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGGCTGGAGCCCTCTGAGAGGGGGCCCCAGGTCTCCATGGCACCTCCGAAGGG 3414
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3415 GCTGGCTCCGATGATTTGATGTGACCTGGGAATGGGGCAGCAGAGGGGCTGCAAGC 3474
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3475 CTCCCCACACATACCCCGCCCTCTACAGCGGTACAGTGAGGACCCCAAGTACCCCTG 3534
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QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCCTCTGAGACTGATGGCTAGCTTGCCCCCTGACCTGCAGCCCCCAGCCTGAATATGTG 3594
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACACGCCAGATGTTCCGGCCCCCAGCCCCCTTCGCCCGAGAGGGCCCTCTGCCTGTGCC 3654
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGCTGTGGTCCACTCTGGNAAGGCCCAAGACTCTCTCCCGAGGGAAGATGGGCTC 3714
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAAAGACGTTTTTGGCTTTGGGGGTGCGTGGAGAACCCCGAGTACTTGCACCCAG 3774
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGCTGCCCTCAGCCCCCACCCTCTCTCCCTTCAGCCAGCCTTCGACAACTC 3834
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGGACCAAGACCCACCAGAGCGGGGGGCTCCACCCAGACCTTCAAGGGGACA 3894
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTAGCCAGAGAAACCAAGACTACCTGGGTCTGGAGCTGCCAGTG 3939
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RESULT 8

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US-10-101-510-81
; Sequence 81, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-81
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Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 15 Gaps: 1
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US-09-493-480-6 (1-919) x US-10-101-510-81 (1-4473)

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QY 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 175 ATGGAGCTGGCGCCTTGTGCCGCTGGGGCTCTCTCGCCCTCTTGGCCCCCGAGCC 234
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCAGTCCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCCAGCTGGACATGCTCCGCCACCTCTACAGGGGTGCCAGGTGGTGCAGGGAAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
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Db	355	GAACCTACCTACCTGCCCCACCAATGCAGCGCTGCTCTCTCCAGGATATCCAGGAGGTG	1435	GACCTCAGCGTCTTCCAGAACTGCAAGTAATCCGGGAGCAAAATCTGCACAAATGGCGCC
Qy	81	GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu
Db	415	CAGGGCTACGTGCTCATCGCTCACACCAAGTGAGCGAGTCCCACTGCAGAGGCTGCGG	1495	TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTACTAGGGAA
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal
Db	475	ATTGTCGAGGACCCAGCTCTTTGAGGACAATATGCCCTGGCCGTGTACACAATGGA	1555	CTGGCAGTGGACTGGCCCTCATCCACCATAACCCACCTCTGCTTCGTGTCACAGGTG
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	481	ProThrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro
Db	535	GACCCGCTGAACATACCAACCCCTGTGCACAGGGCCCTCCCAAGGAGGCTGCGGAGCTG	1615	CCCTGGGACCAAGCTCTTTCCGAAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA
Qy	141	GlnLeuArgSerLeuThrGlnIleLeuLysGlyValLeuIleGlnArgAsnProGln	501	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys
Db	595	CAGCTTCGAAGCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCCCAG	1675	GAGGACGAGTGTGTGGCGAGGGCTGTGCCTGCCACCACTGTGGCCCGAGGGGCACTGC
Qy	161	LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla	521	TyrGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys
Db	655	CTCTGCTACAGACACGATTTTGTGAAGAGACATCTTCCAAAGAACCAACAGCTGGCT	1735	TGGGGTCCAGGGCCCAACCCAGTGTCTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys
Db	715	CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTAAAG	1795	GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGT
Qy	201	GlySerArgCysTyrTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu
Db	775	GGCTCCCGTGTGGGAGAGAGATTCTGAGGATTTGTCTGAGAGCTGCAGAGCTGCAGCGCACTGTCTGT	1855	TTGCCGTGCCACCCCTGAGTGTGAGCCCAAGAAATGCTCAGTGACCTGTTTTGGACCGGAG
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
Db	835	GCCGTGGCTGTGCCCGCTGCAGAGGGCCACTGCCCACTGACTGTGCCCATGAGCAGTGT	1915	GCTGACCACTGTGTGGCTGTGCCCACTATATAGGACCCTCCCTTCTGCGTGGCCCGCTGC
Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTyrPheProAspGluGlu
Db	895	GCTGCCGGCTGCAGCGGCCCAAGCACTCTGACTGCTGCTGCTGCCCTCCCTCAACCAAC	1975	CCCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys
Db	955	AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTACCTACACACACACGCTTTGAG	2035	GGCGATGCCACCTTGCCCCATCAACTGACCCCACTCTCTGTGTGACCTGATGACAAG
Qy	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer
Db	1015	TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGGCCAGCTGTGTGACTGCTGCTGCC	2095	GGCTGCCCGCGAGCAGAGAGCCAGCCCTCTGACGTCCATCATCTCTGCGGTGTGGC
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	653	-----
Db	1075	TACAACTACCTTTCTACGGACGTGGATCCTGCACCCCTGCTGCCCCCTGCACAAACCAA	2155	ATTCTGCTGCTGTGTGCTGTGGGGTGGTCTTTTGGGATCTCTCATCAAGCGACGGCAGCAG
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	653	-----
Db	1135	GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAAGTGCAGCAAGCCCTGTGCCCGA	2215	AAGATCCGGAAGTACACGATGGGGAGACTGTGTGAGGAAACGGAGCTGTGTGAGCGCGCTG
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	653	-----
Db	1195	GTGTGCTATGGTCTGGGCATGAGCACTTCGAGAGGTGAGGCGAGTTACCACTGCCAAT	2275	ACACCTAGCGGAGCGATGCCCAACCGAGCGCAGATGCCGATCCTGAAAGAGACGGAGCTG
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	653	-----
Db	1255	ATCCAGGAGTTTGTGGCTGCAAGAAGATCTTTGGGAGCTGGCATTTCTGCGCGAGAGC	2335	AGGAAAGTGAAGTGTCTGGATCTGGCGCTTTTGGCAGACAGTCTACAAGGGGCATCTGGATC
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	653	-----
Db	1315	TTTGATGGGGACCCAGCCCTCCAAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	2395	CCTGATGGGGAATGTGAAAATTCCAGTGGCCATCAAAAGTGTGTGAGGAAACACATCC
Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	653	-----
Db	1375	GAGACTCTGGAGAGATCAAGGTTACCTATACATCTGAGCATGGCCGAGCAGCTGCCT	2455	CCCAAAGCCAAAGAAATCTTAGACGAAGCATAGCTGATGGTGTGTGGGCTCCCCCA
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	653	-----
			2515	TATGTCTCCCGCTTCTGGGCATCTGCGTCATCAACGGTGCAGCTGTGTGACACAGCTT

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QY 653 ----- 653
Db 2575 ATGCCTATGGCTCTTTAGACCATGTCCGGGAAACCGCGAGCCCTGGGCTCCAG 2634
QY 653 ----- 653
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QY 653 ----- 653
Db 2695 CTGTTACACAGGGACTTGGCGCTCGGAACGTGTGCTCAAGAGTCCCAACCATGTCAAA 2754
QY 653 ----- 653
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QY 653 ----- 653
Db 2815 GGGGGCNAAGTGCCTCAAGTGGATGGCGCTGGAGTCCATTTCTCGCGCGCGGTTCAAC 2874
QY 653 ----- 653
Db 2875 CACCAGAGTATGTGAGGTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934
QY 653 ----- 653
Db 2935 AAACCTTACGATGGATCCCGCGGAGATCCCTGACCTGCTGGAAAGGGGAGCGG 2994
QY 653 ----- 653
Db 2995 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAATGTGGATG 3054
QY 653 ----- 653
Db 3055 ATTGACTCTGAATGTGGCCCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 3114
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGGACCCCCAGCGCTTTGTGTCATCCAGAATGAGGACTTGGGCCCGAGCAGTCCCTTG 3174
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGACCTTCTACCGCTCACGTGCGAGGAGATGACATGGGGACCTGGTGGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTACCCAGGAGGGCTTCTTGTCCAGACCTGCCCCGGGGCTGGG 3294
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3295 GGCATGTCTCCACACAGGCACCGCAGCTCATCTACCAGGAGTGGCGTGGGACCTTGACA 3354
QY 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGGCTGGAGCCCTCTGAAGAGGAGGGCCCCAGAGTCTCCACTGGCACCTCCGAAGGG 3414
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyLeuGlnSer 764
Db 3415 GCTGGCTCCGATGATTTGATGTGTACCTGGGAATGGGGCAGCCCAAGGGGCTGCAAGC 3474
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3475 CTCCCCACATGACCCACGCCCTCTACAGCGGTACAGTGAGGACCCCAAGTACCCCTG 3534
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCTCTGAGACTGATGGTACGTGGCCCCCTGACCTGCAGCCCCCAGCGCTGAATATGTG 3594
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACACGCCAGATGTTGGGCCCCAGCCCCCTTTCGCCCGAGAGGGCCCTCTGCTGCTGCC 3654
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QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
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QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAGAAGCTTTTGGCTTTGGGGTGCCTGGAGAACCCCGAGTACTTGCACCCAG 3774
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGCTGCCCTCAGCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3834
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGGACAGGACCCACAGAGCGGGGGCTCCACCCAGCACCTTTCAAAGGACA 3894
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGGCAGAGAACCCAGAGTACCTTGGGTCTGGACGTGCCAGTG 3939

RESULT 9
US-10-762-128-5
; Sequence 5, Application US/10762128
; Publication No. US20040219161A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409C1
; CURRENT APPLICATION NUMBER: US/10/762,128
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 09/441,411
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-762-128-5

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 20 Gaps: 1

US-09-493-480-6 (1-919) x US-10-762-128-5 (1-4473)

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Db 175 ATGGAGCTGGCGGCTTGTGGCGCTGGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 234
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCGAGGACCCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGGCTCTCTCTCTCTCTCT 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnAsnLeu 60
Db 295 ACCACCTCGACATGTCTCGCCCACTCTACCAGGGCTGCGAGGTGGTGGCAGGGAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspLeuGlnGluVal 80
Db 355 GAACTCACCTACCTGCCCCCAATGCGAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 414
QY 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTACGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 474
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QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
DB 475 ATTGTGGAGGACCCAGCTCTTTGAGGACAACCTATGCCCTGGCGTGTAGACAATGGA 534
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 535 GACCCGCTGAACAATACCAACCCCTGTGTACAGGGGCTCCCGAGGAGCTGGGAGCTG 594
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 595 CAGCTTCGAAGCCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGGGAAACCCCGAG 654
QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
DB 655 CTCGTGTACAGGACACAGATTTTGTGGAAGGACATCTTCCACAAGAACAACAGCTGGCT 714
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 715 CTCACACTGATAGACACCAACCGCTCTCGGGGCTGCGACCCCTGTTCTCCGATGTGAAG 774
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 775 GGCTCCCGCTGTGGGAGAGATTCTGAGGATTGTGAGAGCTGACGGCCTGACGGCCTGTCTGT 834
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
DB 835 GCCGTGGCTGTGCCGCTGCAAGGGGCCACTGCCACTGACTGCTGCCATGAGCAGTGT 894
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 895 GGTGCCGCTGACAGGGGCCCAAGCACCTGACTGCTGCCCTGGCTCCACTTCAACCAC 954
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 955 AGTGGCATCTGTGAGCTGCACTGCCAGGCCCTGGTCACTCAACACAGACACGTTTGAG 1014
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 1015 TCCATGCCCAATCCGAGGCGCGGTATACATTCCGGCGCCAGCTGTGTGACTGCCCTGTCCC 1074
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 1075 TACAACCTACTTTCTACGGACGTGGGACTCTGCACCCCTGCTGCGCCCTGCACAACCAA 1134
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 1135 GAGGTGACAGCAGAGATGCAACACAGCGGTGTGAGAAGTGCAGCAGCCCTGTGCCCGA 1194
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1195 GTGTGCTATGGTCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACCAGTGCCTAAT 1254
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1255 ATCCAGGAGTGTGCTGGGTGCAAGAAGATCTTTGGGAGCGTGGCATTTCTCGCGGAGAGC 1314
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
DB 1315 TTTGATGGGGACCCAGCCTCCAAACACTGCCCGCGCTCCAGCCAGAGCAGCTCCAAGTGT 1374
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
DB 1375 GAGACTCTGGAAGAGATCACAGTTTACCTATATACATCTCAGCATGGCCGAGCAGCTGCCT 1434
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1435 GACCTCAGCGCTCTCCAGAACCTGCAAGTAATCCGGGGAGCGAATTTCTGCACAATGGCGCC 1494
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1495 TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGGAA 1554
QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuLeuCysPheValHisThrVal 480

DB 1555 CTGGCAGTGGACTGGCCCTCATCCACCATAACCCACCTCTGCTTCGTGCACACGGTG 1614
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1615 CCCTGGGACCAAGCTCTTTGGAAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1674
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuLeuCysAlaArgGlyHisCys 520
DB 1675 GAGGACGAGTGTGTGGCGAGGGCCTGGCCTGCCACACAGCTGTGCGCCGAGGGCACTGC 1734
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1735 TGGGTCCAGGGCCACCCAGTGTGTCAACTGCAGCCAGTTCTCTTCGGGGCCAGGAGTGC 1794
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1795 GTGGAGGAATCCGAGTACTGCAGGGGTCCCCAGGAGTATGTGAATCCAGGCACTGT 1854
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1855 TTGCCGTGCCACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1914
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPropheCysValAlaArgCys 600
DB 1915 GCTGACCAAGTGTGGCCTGTGCCCACTATAAGGACCCCTCTCTGCTGGCGCCGCTGC 1974
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
DB 1975 CCCAGCGTGTGAACCTGACCTCTCATACATGCCCATCTCGAAGTTTCCAGATGAGGAG 2034
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
DB 2035 GSCGATGCCAGCTTGCCCCATCACTCACTGACCCACTCTCTGTGTGAGCTGTGATGACAA 2094
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
DB 2095 GSCCTCCCGCGCAGCAGAGAGCCCTCTGACGTCCATCATCTCTGCGTGGTGGC 2154
QY 653 ----- 653
DB 2155 ATCTGCTGGTGGTGGTCTTTGGGGTGGTCTTTGGGATCCTCATCAGCGACGGCAGCAG 2214
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DB 2215 AAGATCCGGAAGTACACGATGCGGAGACTGTCTGCAGGAAAACGAGCTGTGTGGAGCGCTG 2274
QY 653 ----- 653
DB 2275 ACACCTAGCGGAGCGATGCCCAACGAGCGCAGATGCCGATCCTGAAAGAGACGGAGCTG 2334
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DB 2335 AGGAAGGTGAAGTGGTCTGGATCTGGCGTCTTTGGCACAGTCTACNAGGGCATCTGGATC 2394
QY 653 ----- 653
DB 2395 CCTGATGGGAGAAATGTGAARAATCCAGTGGCCATCAAAGTGTGTGAGGGAACACATCC 2454
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DB 2455 CCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGCTCCCCA 2514
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DB 2515 TATGTCTCCGCTTCTGGGCATCTGGCTGACATCCACGGTGCAGCTGTGTGACACAGCTT 2574
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DB 2575 ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCGCGGACGCTGTGGCTCCCCA 2634
QY 653 ----- 653

Db 2635 GACCTGCTGAACGTGTATGTCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2694
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Db 2695 CTCGTACACAGGACTTGGCGCTCGGAACGTGTGCTCAAGAGTCCCAACCATGTCAAA 2754
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Db 2995 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAATGTTGGATG 3054
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Db 3055 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGATGGCC 3114
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGGACCCCCAGCGCTTTGTGTGTCATCCAGAATGAGGACTTGGGCCCGAGCCAGTCCCTTG 3174
Qy 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGACCTTCTACCCCTCCTGCTGGAGGACATGACATGGGGGACCTGGTGGATGCT 3234
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTACCCAGCAGGGCTTCTTGTCTCAGACCTGCCCCGGCGCTGGG 3294
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3295 GGCAATGCTCCACCACAGCCAGCCAGCTCATCTACCAGGAGTGGCGGTGGGACCTGCAC 3354
Qy 725 LeuGluLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCGCCAGGTCTCCACTGGCACCCTCCGAAGGG 3414
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3415 GCTGGCTCCGATGTTATGTTGATGTGACTGGGAATGGGGAGCCAGCGGCTGCAAGC 3474
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3475 CTCCCCACACATACCCCGCCCTCTACAGCGGTACAGTGAGGACCCACAGTACCCCTG 3534
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCCTCTGAGACTGATGCTACGTTGCCCCCTGACCTGCGAGCCCCAGCTGAAATATGTG 3594
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACCGCCAGATGTTCCGCCCCAGCCCCCTTCGCCCCGAGAGGGCCCTCTGCTGCTGCC 3654
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGCTGGTCCACTCTCGAAGAGGCCCAAGACTCTCTCCCCAGGGAAGAAATGGGGTC 3714
Qy 845 ValIleAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAGACGCTTTTGTGCTTTGGGGTGGCGTGGAGAACCCCCGAGTACTTTGACACCCCG 3774

Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGTGCCTCCTCAGCCCAACCTCTCTCTGCTTACGCCAGCTTTCGACAACCTC 3834
Qy 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGACACAGGACCCACAGAGCGGGGGCTCCACCCAGCACCTTTCAAGGGACA 3894
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGGCAGAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3939

RESULT 10

US-10-723-860-8
; Sequence 8, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-8

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 20 Gaps: 1

US-09-493-480-6 (1-919) x US-10-723-860-8 (1-4473)

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Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCGAGACCAAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCCTGCCAGTCCCGAG 294
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnAsnLeu 60
Db 295 ACCACCTCGACATGTCTCGCCACCTCTACAGGGGTGCCAGGTGTGTGCGGGAACCTG 354
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACTCACCTTACCTGCGCCCAATGTCAGCTGTCTCTCTGAGGATATCCAGAGGGTG 414
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTACGTGCTCATCGCTCACACCAAGTGGGAGGTCCCACTGCGAGGGCTGCGG 474
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 475 ATTGTGCGAGGACCCAGCTCTTTGAGGACCAATATGCGCTGCGCGCTGTAGACATGGA 534
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 535 GACCCCTGAAACAATAACACCCCTGTCTACAGGGGCTTCCCGAGAGGCTTGGCGGAGCTG 594

QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValIleuIleGlnArgAsnProGln	160
DB	595	CAGCTTCGAAGCCTCAGAGATCTTGAAGAGGGGCTCTTGATCCAGCGGAACCCCCAG	654
QY	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
DB	655	CTCTGCTACCAGGACAGATTTTGTGAAGGACATCTTCACAAAGAACACAGCTGGCT	714
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	715	CTCACACTGATAGACCAACACGCTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAAG	774
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
DB	775	GGCTCCCGCTGCTGGGAGAGAGATTCTGAGGATTGTGAGAGCCTGACGGCCTGTCGT	834
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisSGluGlnCys	240
DB	835	GCCGCTGGCTGTGCCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT	894
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	895	GCTGCCGGCTGCACGGGGCCCAAGCACTCTGACTGCTGCGCTGCCCTCCACTTCAACCAC	954
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
DB	955	AGTGGCATCTGTGAGCTGCACCTGCCCGCCCTGGTCACCTACAAACAGACAGCTTTGAG	1014
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
DB	1015	TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGGGCCAGCTGTGTGACTGCCGTGCC	1074
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	1075	TACAACTACTCTTTCTACGACGCTGGGATCTCTGCACCCCTCTGTGCCCCCTGCACACCAA	1134
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
DB	1135	GAGGTGACAGCAGAGATGGAAACACACACGCGTGTGAGAACTGACAGAACCCCTGTGCCCGA	1194
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1195	GTGTGCTATGGTCTGGGCTGGAGCACTTGCAGAGGTGAGGGCAGTTACCAAGTGCCAAT	1254
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1255	ATCCAGGAGTTTGTGGCTGCAAGAAAGATCTTTGGGAGCCTGGCATTTCTGCGGGAGAGC	1314
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnValPhe	400
DB	1315	TTTGATGGGGACCCAGCCCTCCAACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1374
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
DB	1375	GAGACTCTGGAAGAGATCACAGGTTACCTATATACATCTCAGCATGGCCGACAGCCTGCCT	1434
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	1435	GACCTCAGCGCTCTTCAGAACCTTGAAGTAATCCGGGGGACGAATTCCTGCACAAATGGCGCC	1494
QY	441	TyrSerLeuThrLeuGlnGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1495	TACTCGCTGACCTTGAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGGAA	1554
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
DB	1555	CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACTCTCTGCTTCGTGCACACGGTG	1614
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	1615	CCCTGGGACAGCTCTTTCCGAACCCGACCAAGCTCTCTCCACTGCCAACCGGCCA	1674

QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	1675	GAGGACGAGTGTGTGGCGAGGGCCTGGCCTGCCACAGCTGTGCCCGGAGGGCACTGC	1734
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	1735	TGGGGTCCAGGGCCCAACCCAGTGTGTAACATGCAGCAGTTCTTCGGGGCCAGGAGTGC	1794
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
DB	1795	GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCGAGGGAGTATGTGAATCCAGGCACTGT	1854
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	1855	TTGCCGTGCCACCCCTGAGGTGCAGCCCCAGAAATGGCTCAGTCACCTGTTTGGACCGGAG	1914
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
DB	1915	GCTGACCAAGTGTGGCCTGTGCCACTATAAGGACCCCTCCCTTCTGCGTGGCCGCTGC	1974
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
DB	1975	CCACGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	2034
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
DB	2035	GGCGCATGCCAGCTTGGCCCATCACTGCACCCCACTCTCTGTGTGGACCTGGATGACAAG	2094
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
DB	2095	GGCTGCCCGCGGAGCAGAGAGCCAGCCCTCTGAGCTCCATCATCTCTCGGTTGGTTGGC	2154
QY	653	-----	653
DB	2155	ATTTCTGCTGTCGTGGTCTTTGGGGTGGTCTTTTGGGATCCTCATCAAGCGACGGCAGCAG	2214
QY	653	-----	653
DB	2215	AAGATCCGGAAGTACACGATGCGGAGACTGTCTGCAGGAAACGGAGCTGTTGGAGCGCTG	2274
QY	653	-----	653
DB	2275	ACACCTAGCGGAGCGATGCCAACAGCGCAGATGCGGATCCTGAAAGAGACGAGCTG	2334
QY	653	-----	653
DB	2335	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGGCATCTGGATC	2394
QY	653	-----	653
DB	2395	CCTGATGGGAGAATGTGAAAATTCAGTGGCCATCAAAGTGTGTAGGGAAACACATCC	2454
QY	653	-----	653
DB	2455	CCCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	2514
QY	653	-----	653
DB	2515	TATGTCTCCCGCTTCTTGGGCATCTGCCCTGACATCCACGGTGCAGCTGTGTGACACAGCTT	2574
QY	653	-----	653
DB	2575	ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCCGCGAGCCCTGGGCTCCAG	2634
QY	653	-----	653
DB	2635	GACCTGCTGAAGTGTGTATGCAGATTGCCAAGGGGATGAGTACTCCTGGAGGATGTGCGG	2694
QY	653	-----	653
DB	2695	CTCGTACACAGGGACTTGGCCGCTCGGAACGTGTGTTCTCAGAGTCCCCAACCATGTCAA	2754
QY	653	-----	653

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Db 2815 GGGGCAAGTGGCCATCAAGTGGATGGCGTGGAGTCCATTCTCCGCGCGGCTTACC 2874
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Db 2875 CACCAGAGTGATGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934
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Db 2935 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTGGAAAGGGGAGCGG 2994
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Db 2995 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGGTCAATGTGGATG 3054
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Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGACCCCGAGCGCTTTGTGGTTCATCCGAATGAGGACTTGGGCGCCAGCGTCCCTTG 3174
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGCACCTTCTACCGCTCACTGCTGAGGACGATGACATGGGACCTGGTGGATGCT 3234
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Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
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Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGCTCGAGCCCTCTGAAGAGGAGGCCCCAGGCTCTCCATGGACCCCTCGAAGG 3414
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Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCANAGACGTTTTTGGCTTTGGGGTGGCGTGGAGNACCCCGAGTACTTGGACACCCAG 3774
Qy 865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 884
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Qy 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904

Db 3835 TATTACTGGACACGAGACCCACGAGCGGGGGCTCCACCCAGCACCTTCAAAGGGACA 3894
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RESULT 11
US-10-207-498-5
; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; FILE REFERENCE: 30448 103-US-UI
; CURRENT APPLICATION NUMBER: US/10/207,498
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-207-498-5
Alignment Scores:
Pred. No.: 0 Length: 3765
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 15 Gaps: 1
US-09-493-480-6 (1-919) x US-10-207-498-5 (1-3765)
Qy 1 MetGluLeuAlaAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTGTGCGGCTGGGGCTCTCTCTGCGGCTCTTGTGCGCGGAGCC 60
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAAGTGTGCAACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGGACATGTCTCGCCACCTCTACAGGGGTGCCAGGTGGTGCGGGAAACTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACTCACCTACCTGCGCCCAATGCGAGCTCTCTCTCTGCGAGGATATCCAGGAGGTG 240
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGCTCATCGCTCAACCAAGTGGAGGCTGCCACTGCCAGAGGCTCGGG 300
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTCGGAGGACCCAGCTCTTTGAGGACAACTATGCTCCCTGCGCGCTGTAGACATGGA 360
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAAATACCAACCCCTGTACAGGGGCTTCCCGAGGAGGCTCGGGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160

Db 421 CAGCTTCGAAGCCTCACAGAGATCTTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG 480
Qy 161 LeuCyseTyrGlnAspThrIleLeuTpyLysAspIlePheHisLysAsnGlnLeuAla 180
Db 481 CTCGTCTACAGGACACGATTTTGTGGAAGGACATCTTCCAAAGAACCAACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCyseHisProCyseSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCACCCCTGTCTCTCGATGTGAAG 600
Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGTCCCGCTGTGGGAGAGATTCTGAGGATTTGTAGAGTTGTAGAGCTGACGGCGCACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 661 GCGGTGGGTGTGCCCGCTGCAAGGGCCACTGTGCCACTGACTGTCTGCCATGAGCAGTGT 720
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGTCTGGCTGTCTCCACTTCAACCA 780
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACCTACAACACAGACACGTTTGAG 840
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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Db 3721 CCTACGCGAGAAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3765
RESULT 12
US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; TITLE OF INVENTION: ANTI-BODY-WAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT. 073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-123-8
Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 9 Gaps: 1
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US-09-811-115-2

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; Patent No. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-811-115-2
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Pred. No.: 0 Length: 3768
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
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QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 781 AGTGGCATCTGTAGCTGCACCTGCCAGCCCTGGTCACTAACACACACACACGTTTGAG 840
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyValSerCysValThrAlaCysPro 300
DB 841 TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGGCCAGCTGTGTGACTGCCCTGTCCC 900
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 901 TACAACCTACCTTCTACGGACGTGGATCCTGCACCCCTCGTCTGCCCTGCACAAACCAA 960
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 961 GAGGTGACAGCAGAGATGGAACACAGCGGTGTGAGAGTGCAGAACGCCCTGTGCCCGA 1020
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1021 GTGTGCTATGGTCTGGGCATGAGCACTTGCAGAGGTGAGGGCAGTTACCACTGCCCAAT 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1081 ATCCAGGAGTTTGTGGCTGCAAGAAGATCTTTGGAGCGTGGCATTTCTGCCGGAGAGC 1140
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1141 TTTGATGGGGACCCAGCCCTCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
DB 1201 GAGACTCTGGAGAGATCACAGGTTACCTATACATCTCAGCATGCGCGGACAGCTGCT 1260
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1261 GACCTCAGCGTCTTCAGAACCTGCAAGTAATCCGGGAGCAATCTGCACAAATGGCGCC 1320
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
DB 1321 TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCACTGAGGGAA 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGCACTGGAGTGGCCCTCATCCACCATACACCCACTCTGCTTCGTGCACACGGTG 1440
QY 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCTGGGACAGCTCTTTCCGAACCCGACCAAGCTCTGCTCCACTGCCAACCGGCCA 1500
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACGAGTGTGGGGCAGGGCTGGCTGCCACCCAGCTGTGGCCCGAGGGCACTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGGTCCAGGGCCACCCAGTGTGTCACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
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QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1681 TTGCCGTGCCACCCCTAGTGTGAGCCCCAGAAATGGCTCAGTCACTGTTTGGACGGAG 1740

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QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
DB 1801 CCCACGGTGTGAACCTGACCTCTCTACATGCCCATCTCGAAGTTTCCAGATGAGGAG 1860
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
DB 1861 GCGCATGCCAGCCTTGGCCCATCACTGCACCCACTCTCTGTGTGACCTGATGACAG 1920
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer- 653
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Db 2821 CTGCCCCAGCCCCCATCTCGACCATTTGATGTCTACATGATCATGTGTCAAATGTTGATG 2880
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Db 2881 ATTGACTCTGAATGTCGGCCAGAGATTCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGAGCCCCCAGCGCTTTGTGGTCTATCCAGAAATGAGGACTTGGGCCCGCAGCAGTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGACCTTCTACCGCTCCTGCTGGAGGAGATGACATGGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
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QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCAGCCAGATGTTGGGCCCGACGCCCTTCCGCCGAGAGGGCCCTCTGCCTGTGCC 3480
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLyThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGCTGCCACTCTGGAAGGGGCCCAAGACTCTCTCCCGAGGAAGATGGGTC 3540
QY 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
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QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGTGGCCCTCAGCCCGCCACCTCTCTCTGCTTACGCCAGCCCTTCGACACCTC 3660
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
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QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAACCAGAGTACTTGGGTCTGGAGTGGCCAGTG 3765
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RESULT 14

US-09-984-092-3

; Sequence 3, Application US/09984092

; Publication No. US20040037840A1

; GENERAL INFORMATION:

; APPLICANT: Pharmexa A/S

; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS

; FILE REFERENCE: P1011PC00

; CURRENT APPLICATION NUMBER: US/09/984,092

; CURRENT FILING DATE: 2001-10-26

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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
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; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
; US-09-984-092-3
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Alignment Scores:

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Pred. No.: 0 Length: 3768
Score: 4992.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 11 Gaps: 1
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US-09-493-480-6 (1-919) x US-09-984-092-3 (1-3768)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGGCGCTCCCTGCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCCACTGGACATGTCTCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGAAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACCTACCTACTGCGCCCAATGCGAGCTGTCTCTCTGAGGATATCCAGGAGGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGTGTCTATCGCTCACACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGACAAATGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAAACATATACACCCCTGTGCAGGGGGCTTCCAGAGGCGCTGCGGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCTCTACAGAGATCTTGAAGAGAGGGGTCTTGATCCAGCGGAACCCCGAG 480
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCCTGTACACAGACACGATTTGTGAAGAGACATCTTCCACAAAGAACCAACAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTTGCAACCCCTGTTCTCCGATGTGTAG 600
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGTCTGGGGAGAGAGTCTGAGGATTTGTGAGGCTGTGAGGCTGTGAGGCTGT 660
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 661 GCGGTGGCTGTGCGCGCTGCAAGGGGGCCACTGCCCACTGCTGCTGCTGCTGCTGCTGCT 720
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGGCTGCACGGGGCCCCAAGCACTCTGACTGTGCTGCTGCTGCTGCTGCTGCTGCT 780
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QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	Db	1861	GGCGCATGCCAGCCTTGCCCATCAACTCACTCCTGTGTGGACCTGGATGACAAG	1920
Db	781	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACCTACACACACACACAGCTTTGAG	840	QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300	Db	1921	GGTCCCCCGCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGCGGTGGTTGCG	1980
Db	841	TCCATGCCCAATCCCGAGGCGCGGTATACATTCGGCGCCAGCTGTGTGACTGCCTGTGCC	900	QY	653	-----	653
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	Db	1981	ATTCTGCTGGTCTGGTCTTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	2040
Db	901	TACAACTACTCTTCTACCGACGTGGATCCTGTACCCTCGTCTGCCCTCGTCGACAAACAA	960	QY	653	-----	653
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	Db	2041	AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGTGTGGAGCGCTG	2100
Db	961	GAGGTGCACAGCAGAGGATGGAACACACAGCGGTGTGAGAACTGCAGCAAGCCCTGTGCCGA	1020	QY	653	-----	653
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	Db	2101	ACACCTAGCGGAGCGATGCCAAACGAGGCGCAGATGCCGATCCTGAAAGAGACGGAGCTG	2160
Db	1021	GTGTGCTATGGTCTGGGCATGGAGCACTTGCAGAGAGTGGGCGAGTTACCAGTGCCTAT	1080	QY	653	-----	653
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	Db	2161	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACNAGGGCATCTGGATC	2220
Db	1081	ATCCAGAGTTTGTCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCGCGAGAGC	1140	QY	653	-----	653
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe	400	Db	2221	CCTGATGGGAGAATGTGAAAATTCAGTGGCCATCAAAGTGTGTAGGGAAAAACACATCC	2280
Db	1141	TTTGTATGGGACCCAGCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1200	QY	653	-----	653
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	Db	2281	CCCAAAGCAAAGAANAATCTTAGACGAAGCATACGTGATGGTGGTGGTGGCTCCCCA	2340
Db	1201	GAGACTCTGGAAGAGATCAGAGTTACCTATATACATCTCAGCATGGCGGACAGCCTGCCT	1260	QY	653	-----	653
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	Db	2341	TATGTCTCCGCCTTCTGGGCATCTGGCATCTGCCTGACATCCACGGTGCAGCTGTGTGACAGCTT	2400
Db	1261	GACCTCAGCGTCTTCGAAACCTGCAAGTAATCCGGGAGCAATCTCGCACAAATGGCGCC	1320	QY	653	-----	653
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460	Db	2401	ATGCCCTATGGCTGCTCTTAGACCATCTCGGGAAACCGCGAGCGCTGGGCTCCCA	2460
Db	1321	TACTCGCTGACCTGCAAGGCTGGGCATCAGCTGGCTGGGCTGGCTCACTGAGGAA	1380	QY	653	-----	653
QY	461	LeuGlySerGlyLeuAlaIleHisAsnThrHisLeuCysPheValHisThrVal	480	Db	2461	GACCTGCTGAACACTGTGTATGACAGATTCCCAAGGGATGAGCTACTCTGGAGGATGTGGG	2520
Db	1381	CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCACCTCTGCTTCTGTGCACACGGTG	1440	QY	653	-----	653
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	Db	2521	CTCGTACACAGGGACTTGGCCGCTCGGAACGTGTGTGTTCAAGAGTCCCACCATGTCAA	2580
Db	1441	CCCTGGGACAGCTCTTTTCGGAACCCGACCAAGCTCTGCTCCACTGCCAACCGGCCA	1500	QY	653	-----	653
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	Db	2581	ATTACAGACTTCGGGCTGGCTGGCTGGACATTGACGACAGACAGAGTACCATGCAGAT	2640
Db	1501	GAGGACGAGTGTGTGGCGAGGGCCTGGCCTGCCACCACTGTGGCCCGAGGGCACTGC	1560	QY	653	-----	653
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	Db	2641	GGGGGCAAGGTGCCCATCAAGTGGATGGCGTGGAGTCCATTCTCCGCCGCGGTTCA	2700
Db	1561	TGGGGTCCAGGGCCCAACCCAGTGTGTCAACTGCAGCCAGTTCTCTTGGGGCCAGGAGTG	1620	QY	653	-----	653
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	Db	2701	CACCAGAGTGTGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC	2760
Db	1621	GTGGAGGAATCCGGACTCTGACGGGGCTCCCGCAGGGAGTATGTGAATGCCAGGCACTGT	1680	QY	653	-----	653
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	Db	2761	AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGCTGTGAAAAGGGGAGCGG	2820
Db	1681	TTGCCGTGCCACCTCGAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGGAG	1740	QY	653	-----	653
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600	Db	2821	CTGCCCAAGCCCCCATCTGCACCATTGATGTCTATCATGATCATGGTCAATGTTGGATG	2880
Db	1741	GCTGACCACTGTGTGGCCCTGTGCCACTATAAGGACCCCTTCTTGGCGTGGCCGCTGC	1800	QY	653	-----	653
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620	Db	2881	ATTGACTCTGAATGTGCGCAAGATTCGCGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC	2940
Db	1801	CCAGCGGTGTGAAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	1860	QY	654	-----GlnAsnGluAspLeuGlyProAlaSerProLeu	664
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QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
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QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
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RESULT 15

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US-10-280-576-3
; Sequence 3, Application US/10280576
; Publication No. US2004004405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280,576
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-280-576-3
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Alignment Scores:

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Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 18 Gaps: 1
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US-09-493-480-6 (1-919) x US-10-280-576-3 (1-3768)

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QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGGACATGTCTCCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGGAACCTG 180
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QY 121 AppProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
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QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
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QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
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GenCore version 5.1.6
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Run on: August 3, 2005, 12:34:58 ; Search time 284.625 Seconds
(without alignments)
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Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3776	95.5	3768	4	US-09-811-115-2
4	3776	95.5	4473	2	US-09-048-804-1
5	3776	95.5	4473	3	US-09-056-105-26
6	3776	95.5	4473	4	US-09-663-834A-3
7	3776	95.5	4473	4	US-09-441-411-5
8	3776	95.5	4530	1	US-08-229-515A-9
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10	3776	95.5	4530	3	US-09-167-322-4
11	3776	95.5	4530	4	US-09-527-487-1
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13	3776	95.5	9274	4	US-09-811-115-1	Sequence 1, Appli
14	3632	91.9	2385	2	US-09-146-283-3	Sequence 3, Appli
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17	3471	87.8	1872	3	US-08-422-108-2	Sequence 2, Appli
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19	3205	81.1	3955	1	US-08-229-515A-14	Sequence 14, Appli
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25	1451	36.7	5501	1	US-08-484-438-1	Sequence 1, Appli
26	1451	36.7	5555	1	US-08-484-438-3	Sequence 3, Appli
27	1435	36.3	4905	1	US-07-978-895-3	Sequence 3, Appli
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29	1435	36.3	4905	2	US-08-475-352-3	Sequence 3, Appli
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33	1412	35.7	5687	4	US-09-919-039-268	Sequence 268, App
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37	1032	26.1	1958	4	US-09-867-521-1	Sequence 1, Appli
38	942	23.8	1593	3	US-09-676-610B-25	Sequence 25, Appli
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43	376	9.5	2533	3	US-09-149-922-5	Sequence 5, Appli
44	369.5	9.3	4149	2	US-08-737-715-1	Sequence 1, Appli
45	369.5	9.3	4723	4	US-09-023-655-1137	Sequence 1137, Ap

ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/08625101
; Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

; LENGTH: 3768 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..3765
 US-08-625-101-1

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; Sequence 1, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3768
; OTHER INFORMATION: /note= "product = "cerB-b2""
US-08-356-786-1

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 2 Gaps: 1

US-09-493-480-7 (1-712) x US-08-356-786-1 (1-3768)

QY	1	MetGluLeuAlaAlaLeuCybArgTTPGlyLeuLeuLeuAlaLeuLeuProProGlyAla	20
Db	1	ATGGAGCTGGGGCCCTTGCCGCTGGGGCTCCTCCTCGCCCTCTTGCCCCCGGAGCC	60
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
Db	61	GCAGACCAACAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCTCCAGTCCCGAG	120
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrglnGlyCysGlnValValGlnGlyAsnLeu	60
Db	121	ACCCACCTGGACATGCTCGGCCACCTCTACAGGGCTGCAGGTGGTGGAGGAAACCTG	180
QY	61	GluLeuThrTyrrleuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80
Db	181	GAACCTACCTACTGCCCCCAATGCGCCCTGCTCTCTCTGAGGATATCCAGAGGTG	240
QY	81	GlnGlyTyrrValleuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	241	CAGGGCTAGCTCATCGCTCACACCAAGTGAGGCAGTCCCACCTGCAGAGGCTGCGG	300
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrrAlaLeuAlaValLeuAspAsnGly	120
Db	301	ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGSCCTGCGCGTGTAGACAAATGGA	360
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	361	GAACCGCTGAAACATACCAACCCCTGTACAGGGGCTCCCGAGGAGGCTGCGGAGCTG	420
QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
Db	421	CAGCTTCGAAGCTCACAGAGATCTTTGAAGGAGGGGTCTTGATCCAGCGGAACCCACAG	480
QY	161	LeuCysTyrrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
Db	481	CTCTGTACACGAGACAGATTTGTGGAAGGACATCTTCCACAAGAACCAACAGCTGGCT	540
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	541	CTCACACTGATAGACACCAACCGCTCTCGGGCTCGCCACCCCTGTCTCCGATGTGTAG	600
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	601	GGCTCCGCTGTGGGAGAGATTTCTGAGGATTTGTACAGGCTGACGCGCTGTCTGTCT	660
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys	240
Db	661	GCCGCTGGCTGTGCCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT	720
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	721	GTCGCGGCTGCACGGGCCCAAGCACTCTGACTGCTGGCTGGCTCCACCTTCAACCCAC	780
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrrAsnThrAspThrPheGlu	280
Db	781	AGTGGCATCTGTGAGCTGACTGCCAGCCCTGGTCACTACACACACACACACGCTTTGAG	840
QY	281	SerMetProAsnProGluClyArgTyrrThrPheGlyAlaSerCysValThrAlaCysPro	300
Db	841	TCCATGCCCAATCCCGAGGCGGATATACATTCGGCGCCAGCTGTGTGACTGCTGCTCCC	900
QY	301	TyrAsnTyrrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	901	TACAACTACTTCTACGAGAGCTGGGATCTTGCAACCTCTGTGCCCCCTGCACAAACCA	960
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
Db	961	GAGGTGCACAGCAGAGGATGGAACACAGCGGTGTGAGAAAGTGACGAGGCTGTGCCGA	1020
QY	341	ValCysTyrrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
Db	1021	GTGTGCTATGGTCTGGGCATGGAGCATTTGCCAGAGGTGAGGGCATTTACAGTGCCTAT	1080
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1081	ATCCAGGAGTTTGTCTGGCTGCAGAGAGATCTTTTGGAGGCTTGCACTTTCTGCCGAGAGC	1140
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
Db	1141	TTTGTATGGGACCCAGCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1200
QY	401	GluThrLeuGluGluIleThrGlyTyrrleuTyrrIleSerAlaTrpProAspSerLeuPro	420
Db	1201	GAGACTCTGGAAGAGATCACAGTTTACCTATATCATCTCAGCATGGCCGACAGCCTGCCT	1260
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
Db	1261	GAACCTCAGGCTCTTCCAGAACCTGCAAGTATCCGGGAGCAATCTTGACAAATGGCGCC	1320
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
Db	1321	TACTCGCTGACCTGCAAGGGCTGGCATCAGCTGGCTGGGGCTGCGCTCACTGAGGGAA	1380
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
Db	1381	CTGGCAGTGGACTGGCCCTCATCCACCAATACACCCACCTCTGCTTCGTGCACACGGTG	1440
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
Db	1441	CCCTGGGACCAGCTCTTTGGNAACCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1500
QY	501	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
Db	1501	GAGGACGAGTGTGGGAGGCGCTGGCTGCCACCACTGTCGCCCGCCGAGGGCACTGC	1560
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	1561	TGGGTCACAGGGGCCACCCAGTGTGTCAACTGACGCCAGTTCTCTTGGGGCCAGAGTGC	1620
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrrValAsnAlaArgHisCys	560
Db	1621	GTGGAGGATGCCGAGTACTGCAGGGGCTCCCGACGGAGTATGTGATGCCAGGCACTGT	1680
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
Db	1681	TTGCGCTGCCACCTTGAGTGTGAGCCCAAGATGGCTCAGTGCCTGTTTGGACCGGAG	1740
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrrLysAspProProPheCysValAlaArgCys	600
Db	1741	GCTGACCAAGTGTGGCTGTGCCCACTATAGGACCTTCCCTTCTGCGTGGCCGCTGC	1800
QY	601	ProSerGlyValLysProAspLeuSerTyrrMetProIleTrpLysPheProAspGluGlu	620
Db	1801	CCCAGCGTGTGAACCTGACCTCTCTACATGCCCACTTGGAGTTTCCAGATGAGGAG	1860
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys	640
Db	1861	GGCGCATGCCAGCTTGGCCCCCATCAACTGACCCACTCTCTGTGTGGACCTGGATGACAAG	1920
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	1921	GGCTCCCCCGCAGCAGAGAGCCCTCTGACGTCCATCATCTCTCGGTGGTGTGGC	1980
QY	653	-----	653
Db	1981	ATTCTGCTGGTGTGCTTGGGGGTGGTCTTTGGGATCTCTCAAGCGACGGCAGCAG	2040
QY	653	-----	653
Db	2041	AAGATCCGGAAGTACACGATGCGGAGACTGTCTGCAGGAAACGAGCTGTGTGGAGCGCTG	2100
QY	653	-----	653
Db	2101	ACACCTAGCGGAGCGATGCCCAACCGCGGCAGATGCGGATCTCTGAAAGAGACGAGCTG	2160
QY	653	-----	653

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Db 2161 AGAAGGTGAAGTGTCTGGATCTGGCGCTTTTGGCACAGCTTACAAGGGCATCTGGATC 2220
QY 653 -----
Db 2221 CCTGATGGGAGAAATGTGAAATTCAGTGGCCCATCAAGTGTGTAGGGAACACATCC 2280
QY 653 -----
Db 2281 CCCAAGCCAAACAAGAAATCTTAGACGAAGCATACGTGATGCTGTGTGGGCTCCCCA 2340
QY 653 -----
Db 2341 TATGTCTCCGCTTCTGGGCATCTGCCTGACATCCACGGTGAGTGTGTGACACAGCTT 2400
QY 653 -----
Db 2401 ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCGCGGACGCCTGGGCTCCAG 2460
QY 653 -----
Db 2461 GACCTGTGAATGGTGTATGACAGATTGCCAAGGGATGAGCTACCTGGAGGATGTGGG 2520
QY 653 -----
Db 2521 CTCGTACACAGGAGCTTGGCCGCTCGGAACGTGCTCGAAGTCCCAACCATGTCAA 2580
QY 653 -----
Db 2581 ATTACAGACTTCGGGTGGCTGGCTGGCTGGACATTTGACGAGACAGATACCATGCAGAT 2640
QY 653 -----
Db 2641 GGGGGCAAGGTGCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTCAAC 2700
QY 653 -----
Db 2701 CACCAGATGATGTGGAGTTATGTGTGATGTGTGGAGCTGATGACTTTTGGGGCC 2760
QY 653 -----
Db 2761 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTCTGGAAGGGGAGCGG 2820
QY 653 -----
Db 2821 CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGTGTCAAATGTTGATG 2880
QY 653 -----
Db 2881 ATTGACTCTGAATGTCGGCCCAAGATTCCGGGAGTTGGTGTCTGAAATTTCCCGCATGGCC 2940
QY 654 -----
Db 2941 AGGGACCCCGAGCGCTTTGTGGTATCCAGATGAGACTTTGGGCCAGCAGTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 694
Db 3001 GACAGCACCTTCTACCGCTCACTGCTGGAGACGATGACATGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGGTACCCAGCAGGAGGCTTCTGTCTCCAGACCTGCCCCGGCGCTGGG 3120
QY 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGATGTCTCCACACAGGCAACCCG 3144
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RESULT 3

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US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
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; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811.115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2
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Alignment Scores:

Pred. No.:	0	Length:	3768
Score:	3776.00	Matches:	712
Percent Similarity:	67.94%	Conservative:	0
Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
DB:	4	Gaps:	1

US-09-493-480-7 (1-712) x US-09-811-115-2 (1-3768)

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QY 1 MetGluLeuAlaAlaLeuCysArgTTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTGTGGCGCTGGGGCTCTCTCTCGCCCTCTTGGCCCGGAGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGGACATGTCTCGCCACCTCTACAGGGCTGCCAGGTGTGCAAGGAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACTCACCTACTGCCCCCAATGCCAGCTGTCTCTCTCCAGGATATCCAGGAGGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGTCTATCGCTCACAACTCAAGTGAAGTGGAGTCCCACTGCAGAGGCTCGG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGCAACCCAGCTCTTTGAGGACAACTATGCCCTGGCGCTGTAGACAAATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAAATACCACTCCCTGTCAAGGGGCTCCCCAGGAGGCTCGGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCTCTACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAAACCCCGAG 480
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGTCTACGAGACACGATTTGTGGAAGGACATCTTCCAAAGAACCAACAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAG 600
QY 201 GlySerArgCysTTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGTGGGGAGAGATTTCTGAGGATTTGTGAGAGCTGTGAGAGCTGCTGTGT 660
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 661 GCGGTGGTGTGCTGCCCGCTGCAAGGGGCCACTGCCCCACTGCTGCTGCTGCTGCTGCTG 720
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QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260	QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
Db	721	GTCGCGGCTGCACGGGCCCAAGCACTCTGACTGCTGGCTGCTCCACTTCAACAC	780	Db	1801	CCCACGGTGTGAACCTGACCTCTCTACATGCCCACTTGAAGTTTCCAGATGAGGAG	1860
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLeuLys	640
Db	781	AGTGGCATCTGTGAGCTGCCACTGCCAGCCCTGGTCACCTACAAACACAGACACGTTTGAG	840	Db	1861	GCGCATGCCAGCCTTGCCCATCACTCACTCCATCCCACTCTCTGTGTGGACCTGGATGACAAG	1920
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300	QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	841	TCACATGCCCAATCCGAGGCCGGTATACATTCGCGCCAGCTGTGTGACTGCCCTGTGCC	900	Db	1921	GGCTCCCCCGGAGACAGAGCCGCCCTCTGACGTCCATCGTCTCTCGGTTGTTGGC	1980
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	QY	653	-----	653
Db	901	TACAACTACTTCTACGAGCGTGGGATCTGCACCTCTGCCCCCTGCACAAACCA	960	Db	1981	ATTCTGCTGGTGGTCTTGGGGTGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	2040
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	QY	653	-----	653
Db	961	GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAGGTGAGGCGAGTTACCAAGTGCCAAT	1020	Db	2041	AAGATCCGGAAGTACACGATGCGGAGACTGTCTGCAGGAAACGGAGCTGGTGGAGCGCTG	2100
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	QY	653	-----	653
Db	1021	GTGTGCTATGGTCTGGGCATGAGCACTTGCAGAGGTGAGGCGAGTTACCAAGTGCCAAT	1080	Db	2101	ACACCTAGCGGAGCGATGCCCAACGAGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG	2160
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	QY	653	-----	653
Db	1081	ATCCAGGAGTTTGTGCTGCAGAGAGATCTTTGGGAGCTGGCATTTCTGCGGAGAGC	1140	Db	2161	AGGAAGGTGAAGTCTTGGATCTGGCGTTTGGCACAGTCTACAAGGGCATCTGGATC	2220
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe	400	QY	653	-----	653
Db	1141	TTTGTGGGAGCCAGCCTCCAACCTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1200	Db	2221	CCTGATGGGAGAGTGTGAAATTCAGTGGGCCATCAAAAGTGTGAGGGAACACATCC	2280
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	QY	653	-----	653
Db	1201	GAGACTCTGGAGAGATCACAGGTTACCTATATCATCTCAGCATGGCCGACAGCTGCCT	1260	Db	2281	CCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGGGCTCCCCA	2340
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	QY	653	-----	653
Db	1261	GACCTCAGGCTCTTCAGAACTCTCAGATTAATCCGGGGACGAATCTGCACAAATGGCGCC	1320	Db	2341	TATGTCTCCGCTTCTGGGCATCTGCCTGACATCCACGGTGCAGTGGTGGTGCACAGCTT	2400
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460	QY	653	-----	653
Db	1321	TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGCTGCGCTCACTGAGGAA	1380	Db	2401	ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCCGGGACGCCTGGGCTCCAG	2460
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480	QY	653	-----	653
Db	1381	CTGGGCAGTGGACTGGCCCTCATCCACCATAACCCACCTCTGTCTGTGCACACGGTG	1440	Db	2461	GACCTGTGAACCTGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG	2520
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	QY	653	-----	653
Db	1441	CCCTGGGACCACTCTTTCGGAAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1500	Db	2521	CTCGTACACAGGACTTGGCCGCTCGGAACGTGTGCTCAAGAGTCCCAACCATGTCAAA	2580
QY	501	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	QY	653	-----	653
Db	1501	GAGGACAGTGTGTGGCGGAGGCTGGCTGCCACCACTGTGGCCCGCGGCACTGC	1560	Db	2581	ATTACAGACTTTCGGGCTGGCTGGCTGGGACTTACGAGACAGAGTACCATGCAGAT	2640
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnCys	540	QY	653	-----	653
Db	1561	TGGGTTCAGGGGCCCAACCAAGTGTGTCAACTGCAGCCAGTTCTTGGGGCCGAGAGTGC	1620	Db	2641	GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTTCTCCGCCGGGGTTCAAC	2700
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	QY	653	-----	653
Db	1621	GTGGAGGAATCGGAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT	1680	Db	2701	CACCAGAGTATGTGTGGAGTTTATGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC	2760
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	QY	653	-----	653
Db	1681	TTGGCGTGCCACCCCTGAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGGAG	1740	Db	2761	AAACCTTAGTGGATCCACGCCGGGAGATCCCTGACCTGCTGGAAAAAGGGGAGCGG	2820
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600	QY	653	-----	653
Db	1741	GCTGACCAAGTGTGGCCCTGTGCCCACTATAAGGACCCCTCCCTTCTGCGTGGCCCGCTGC	1800	Db	2821	CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGGTCAAAATGTTGGATG	2880
				QY	653	-----	653

Db 2881 ATTGACTCTGAATGTCGGCCAAAGANTTCGGGAGTTGGTGTCTGTAATTCTCCCGCAGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGAGACCCCGAGCGCTTTGGTGTATCCAGATGAGGACTTGGGCCAGCCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCACTGCTGGAGACGATGACATGGGGACCTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGAGATATCTGGTACCCAGCAGGGCTTCTTGTCTCAGACCCCTGCCCGGGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGCTCCACCACAGCCACCGC 3144

RESULT 4

US-09-048-804-1
; Sequence 1, Application US/09048804
; Patent No. 5968748
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
; TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,804
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Leggaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2913
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4473 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; ANTI-SENSE: No
US-09-048-804-1

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 2 Gaps: 1
US-09-493-480-7 (1-712) x US-09-048-804-1 (1-4473)
Qy 1 MetGluLeuAlaAlaLeuCysArgTTPGlyLeuLeuAlaLeuLeuProProGlyAla 20
Db 175 ATGGAGCTGGCGGCTTGTGCGCGCTGGGGGCTCTCTCGCCCTTGTGCCCGCGAGCC 234

Qy 21 AlaserThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCAGCACCACCAAGTGTGCACCGCACAGACATGAAGCTGGCGTCTCTGCAGTCCCGAG 294
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnVal 60
Db 295 ACCACCTGGACATGTTCGCCACCTCTTACACGGGCTGCCAGGTGGTGGAGGAAACCTG 354
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACTCACCTACCTGCGCCACCAATGCGAGCTGTCTTCTCTGAGGATATCCAGGAGGTG 414
Qy 81 GlnGlyTyrValLeuLeuLeaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTAGTGTCTCATCGCTCAACAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 474
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 475 ATTGTGGAGGCCACCCAGCTCTTTTGAGGACAACTATGCTCCCTGGCGGTGCTAGACAA 534
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 535 GACCCGCTGACACATACCCCTGTGCAGAGGGGCTTCCCGAGGAGGCTTGGGGAGCTG 594
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160
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RESULT 5

US-09-056-105-26
; Sequence 26, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221


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RESULT 6
US-09-663-834A-3
; Sequence 3, Application US/09663834A
; Patent No. 6613567
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
; FILE REFERENCE: RTS-0033
; CURRENT APPLICATION NUMBER: US/09/663,834A
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175) ... (3942)
US-09-663-834A-3

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-7 (1-712) x US-09-663-834A-3 (1-4473)

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641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
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QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
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QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
DB 1375 GAGACTCTGGAGAGATCAGAGTTACTATACATCTCAGCATGGCCGGACAGCTGCCT 1434
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1435 GACCTCAGCGCTCTCCAGAACCTGCAAGTAGTAATCCGGGGACGAATTTCTGCACATGGCGCC 1494
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
DB 1495 TACTCGTGCCTTCCAGGGCTGGGCATCAGCTGGCTGGGGCTGCCTCCTCCTCAGGGAA 1554
QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
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QY 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
DB 1915 GCTGACCAAGTGTGGCTGTGCCACTATAGGACCTCCCTCTGCGTGGCCCGCTGC 1974
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QY 653 653 2275 ACACCTAGCGGAGGATGCCAACCGAGCGCAGATCGGATCTCTGAAGAGACGGAGCTG 2334
QY 653 653 2335 AGGAAGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2394
QY 653 653

DB 2395 CTTGATGGGGAGAAATGTGAAAAATTTCCAGTGGCCCATCAAAAGTGTGTGAGGGAAAAACACATCC 2454
QY 653 653 2455 CCCAAGGCCAACAAAGAAATCTTTAGACGAAGCATACGTGATGGCTGTGTGGGCTCCCCA 2514
DB 653 653 2515 TATGTCTCCCGCTTCTTGGGCATCTGCTTGACATCCACGGTGCAGCTGGTGACACAGCTT 2574
QY 653 653 2575 ATGCCCTATGGCTGCCTCTTTAGACCATGTCCGGGAAAAACCGCGACCGCTGGGCTCCAG 2634
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QY 653 653 2695 CTGCTACACAGGAGCTTGGCGGCTCGGAACGTGCTGTCAAGAGTCCCAACCATGTCAAA 2754
DB 653 653 2755 ATTACAGACTTCCGGCTGGCTCGGCTGTGACATTGACGAGACAGAGTACCATGCGAGAT 2814
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DB 653 653 2875 CACCAGAGTATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2934
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DB 3175 GACAGACACTTCTACCGCTCACTGCTGGAGGACATGACATGGGGACCTGGTGGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3235 GAGGAGTATCTGTGTACCCAGCAGGCGCTTCTTGTCTCAGACCTGTCCCGGGCGCTGGG 3294
QY 705 GlyMetValHisHisArgHisArg 712
DB 3295 GGCATGCTCCACCACAGGCACCGC 3318
RESULT 8
US-08-229-515A-9
; Sequence 9, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, PAZUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19

/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NEEDLE & ROSENBERG PC
/ STREET: 127 Peachtree Street, Suite 1200
/ CITY: Atlanta
/ STATE: Georgia
/ COUNTRY: usa
/ ZIP: 30303
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/229,515A
/ FILING DATE: 19 APR 1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PERRYMAN, DAVID G
/ REGISTRATION NUMBER: 33,438
/ REFERENCE/DOCKET NUMBER: 1414.608
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 404-688-0770
/ TELEFAX: 404-688-9880
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4530 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-229-515A-9

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 1 Gaps: 1

US-09-493-480-7 (1-712) x US-08-229-515A-9 (1-4530)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProhlaSerProGlu 40
DB 211 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTCGGCTCCCTGCCAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 271 ACCACCTGGACATGCTCCGCCACCTCTACCGAGGCTGCAGGTGGTGAGGGAAACCTG 330
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DB 391 CAGGGCTACGTGCTCATCGCTCACACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGGGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
DB 451 ATTGTGGAGGACCCAGCTCTTTGAGGACAACTATGCCCTCGCCCGTGTAGACAACTGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 511 GACCCGCTGAACAATACCAACCCCTGTACAGGGGCTCCCGAGGGCTCCCGAGGAGCTG 570
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DB 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAAG 750
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 751 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGGATTTGTAGAGCTGTGAGCGCACTGTCTGT 810
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DB 811 GCCGCTGGCTGTGCCCGCTGCAAGGGCCACTGCCCACTGCTGCTGCCATGAGCAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 871 GCTGCCGCTGCACGGGCCCAAGCACTCTGACTGCTGCCCTGGCTGCCCTCCACTTCAACCCAC 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 931 AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTACACACACACACAGTTTGAG 990
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
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QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1651 GAGGACAGTGTGTGGGAGGGCCCTGGCTGCCACAGCTGTGGCCCGGAGGCACTGC 1710
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QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
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QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
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QY 653 ----- 653
Db 2131 ATTCTGCTGTGCTGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCAGCGCAGCAG 2190
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Db 2191 AAGATCCGAAGTACACGATGCGGAGACTGCTGCAGGAACGGAGCTGTGTGGAGCCGCTG 2250
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QY 653 ----- 653
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QY 653 ----- 653
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Db 2791 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTTACC 2850
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RESULT 9
US-08-645-865-9
; Sequence 9, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-645-865-9

Alignment Scores:

Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 1 Gaps: 1

US-09-493-480-7 (1-712) x US-08-645-865-9 (1-4530)

QY 1 MetGluLeuAlaLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
DB 151 ATGGAGCTGGCGGCTTGTGGCGCTGGGGCTCTCTCGCCCTCTTGGCCCCCGGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 211 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 271 ACCCACTGGACATGCTCCGCCACCTCTACCAAGGCTGCCAGGTGGTGAGGGAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
DB 331 GAACCTCACCTACTGCCCAACCAATGCCAGCCTGTCTCTCTCCAGGATATCCAGAGGTG 390
QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 391 CAGGGCTAGTGCTCATCGCTCACCAACCAAGTGAGGAGGTGCCAGTCCCATCCAGAGGTG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspGlnGly 120
DB 451 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACATATGCCCTGGCGTGTGTACACAAATGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 511 GACCCGCTGAACAATACCACCCCTGTCCAGGGGCTCCCCAGGAGGCTGCGGAGGTG 570
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 571 CAGCTTCGAAGCCTCACAGAGATCTTGAAGAGGGGTCTTGTATCAGCGGAACCCCGAG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
DB 631 CTCGTCTACGAGACACGATTTTGTGAGAGACATCTTCCACAAAGAACACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGAAG 750
QY 201 GlySerArgCysTrpGlyLysSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 751 GCGTCCCGCTGTGGGAGAGAGATTCTGAGGATTGTCTAGAGCTGACAGCGCTACTGTCTGT 810
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
DB 811 GCGGTGGCTGTGGCGCTGCAAGGGGCCACTGCCCACTGACTGTCTGCCATGAGCAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 871 GCTGCCGCTGCACGGGCCCAAGCACCTGACTGCTGCCCTGGCTGCCCTCCACTTCAACCCAC 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 931 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTACCAACACACACACACGCTTTGAG 990
QY 281 SerMetProAsnProGluGluValArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 991 TCCATGCCCAATCCCGAGGGCCGATATCATTTGGGGCCGAGCTGTGTACTGCCCTGTCCC 1050
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320

DB 1051 TACAACCTACCTTTCTACGGACGTGGGATCTCGACCCCTCGTCTGCCCCCTGCACAACCAA 1110
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 1111 GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGAAGCCCTGTGCCCGA 1170
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1171 GTGTCTATGTCTGGGCATGAGGACCTTGCAGAGGTGAGGGCAGTTACCAAGTGCAT 1230
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1231 ATCCAGGAGTTTGTCTGGCTGCAGAAGATCTTTGGAGGCTCGGCATTTCTGCCGGAGAGC 1290
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1291 TTTGATGGGGACCCAGCCTCCAACATGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1350
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
DB 1351 GAGACTCTGGAAAGAGATCACAGTTTACTATACATCTCAGCATGGCCGACAGCTGCCT 1410
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1411 GACCTCAGCGTCTTCCAGAACCTCGAAGTAATCCGGGACGAATCTGCACAATGGCGCC 1470
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1471 TACTCGCTGACCTCCAAAGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTCCTCAGTGA 1530
QY 461 LeuGlySerGlyLeuAlaLeuIleHisLeuThrHisLeuCysPheValHisThrVal 480
DB 1531 CTGGGCACTGGACTGGCCCTCATCCACCATTAACACCCACTCTCTGCTGTGCACACGGTG 1590
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1591 CCCTGGGACCACTCTTTCCGAACCCCGACCAAGCTCTGCTCCACACTGCCAACCGCCA 1650
QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1651 GAGGACGAGTGTGTGGGCGAGGGCTGGCTGCCACCACTGTGGCGCCGAGGGCACTGC 1710
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1711 TGGGCTCCAGGGCCCAACCCAGTGTCTCAACTGCACCCAGTTCCTTCGGGGCCAGGAGTG 1770
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1771 GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACCTGT 1830
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1831 TTGCGCTGCCACCTGAGTGTGAGGTCAGCCCCAGAAATGCTCAGTACCTGTGTGGACGGAG 1890
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
DB 1891 GCTGACGAGTGTGTGGCTGTGCCCACTATAAGGACCCCTCCCTCTGTGCGTGGCCGCTGC 1950
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
DB 1951 CCCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 2010
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
DB 2011 GCGCATGCCAGCTTGGCCCATCAACTGACCCCACTCTCTGTGTGACCTGTGATGAAG 2070
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
DB 2071 GGCTGCCCGCCGACGAGAGAGCCCTCTGACGTCCATCGTCTCTGCGGTGGTTGGC 2130
QY 653 ----- 653

Db	331	GAACCTCACCTACTCGTCCCAACCAATGCAGCTGTCTCTCTCGAGGATATCCAGGAGGTG	390	Db	1411	GACCTCAGCGTCTTCCAGAAACCTGCAAGTAATCCGGGACGAATTCCTGCACAATGGCGCC	1470
Qy	81	GinGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuClnArgLeuArg	100	Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
Db	391	CAGGGCTACGTGCTCATCGCTCACACCAAGTGAGGCAGGTCCCATCTGCAGAGGTGCGG	450	Db	1471	TACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTGCATCTGAGGGAA	1530
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120	Qy	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
Db	451	ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTACACATGGA	510	Db	1531	CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTCGTGCACACGGTG	1590
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140	Qy	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
Db	511	GACCCGCTGAACAATACCACCCCTGTGCACAGGGCCCTCCCCAGGAGGCTCGGGAGCTG	570	Db	1591	CCCTGGGACCAAGCTTTTCGGAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1650
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160	Qy	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
Db	571	CAGCTTCGAAGCTTCACAGAGATCTTTGAAGAGGGGTCTTGATCCAGCGGAACCCCCAG	630	Db	1651	GAGGACGAGTGTGGCGAGGGCTTGGCCTGCCACCAGCTGTGCCCGAGGGGCACTGC	1710
Qy	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisIleAsnAsnGlnLeuAla	180	Qy	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	631	CTCTGTACACGACACAGATTTTGTGGAAGGACATCTTCCACAGAACCAACAGCTGGCT	690	Db	1711	TGGGCTCCAGGGCCACCACAGTGTCTCAACTGCAGCCAGTTCCTTCGGGGCCAGAGTGC	1770
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200	Qy	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
Db	691	CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAG	750	Db	1771	GTGGAGGAATCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGT	1830
Qy	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220	Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
Db	751	GGCTCCCGCTGTGGGAGAGAGATTCTGAGGATTTGTCAGAGGCTGCAGCGCACTGTCTGT	810	Db	1831	TTGCCGTGCCACCTGAGTGTGAGCCCCAGAAATGGCTCAGTACCTGTTTGGACCGGAG	1890
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240	Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys	600
Db	811	GCGGTGGCTGTGCCGCTGCAAGGGGCCACTGCCCACTGACTGTGCCCATGAGCAGTGT	870	Db	1891	GCTGACCAAGTGTGGCTGTGCCCTGTGCCCACTATAAGGACCCCTCCCTTCTGCGTGC	1950
Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260	Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
Db	871	GCTGCCGGCTGCAGGGCCCCAAGCACTCTGACTGCTGCTGCCCTGCCCTCCACTTCAAC	930	Db	1951	CCCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	2010
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
Db	931	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACCTACAACACAGACACGTTTGAG	990	Db	2011	GGCGATGCCAGCTTGCCCCATCAACTCAACTGCACCCACTCTGTGTGGACCTGATGACAAG	2070
Qy	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300	Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	991	TCCATGCCCAATCCCAGAGGGCCGGTATACATTCGGGCCAGCTGTGTGACTGCTGTCCT	1050	Db	2071	GSGTSCCCCGCGAGCAGAGAGCAGACGCCCTCTGACGTCCATCGTCTCTGCGGTGGTGGC	2130
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	Qy	653	-----	653
Db	1051	TACAACACTACTTCTACGGACGCTGGGATCCTGCACCCCTGCTGCCCCCTGCACAACCAA	1110	Db	2131	ATTCTGCTGTCGTGTCGTCTTGGGGGTGGTCTTTTGGGATCTCTCATCAGCGACGGCAGCAG	2190
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	Qy	653	-----	653
Db	1111	GAGGTACACAGCAGAGATGGAACACAGCGGTGTGAAGTGCAGCAAGCCCTGTGCCCGA	1170	Db	2191	AAGATCCGGAAGTACACGATGCGGAGACTGTGTGAGGAAACGGAGCTGGTGGAGCGCGCTG	2250
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	Qy	653	-----	653
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Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	Qy	653	-----	653
Db	1231	ATCCAGAGTTTGTGCTGGCTGCAAGAAGATCTTTGGGAGGCTGGCATTTCTGCGGAGAGC	1290	Db	2311	AGGAAGTGAAGGTGCTTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGGCATCTGGATC	2370
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe	400	Qy	653	-----	653
Db	1291	TTTGATGGGGACCCAGCCTCCAAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1350	Db	2371	CCTGATGGGGAGATGTGAAATTCAGTGGCCATCAAAAGTGTGGGAAACACATCC	2430
Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	Qy	653	-----	653
Db	1351	GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGACAGCCTGCCT	1410	Db	2431	CCCAAAGCCAAACAAGAAATCTTAGACGAAGCATACGTGATGGTGGTGGCTCCCCA	2490
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	Qy	653	-----	653
				Db	2491	TATGTCTCCCGCCTTCTGGGCATCTGCTGCATCCACGGTGCAGCTGGTGACACAGCTT	2550

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QY 653 ----- 653
Db 2671 CTCGTACACAGGACTTGGCGCTCGGAACGTGCTGCTCAAGAGTCCCAACCATGTCAAA 2730
QY 653 ----- 653
Db 2731 ATTACAGACTTCGGGCTGGCTCGGCTGCTGGACATTCACGAGACAGAGTACCATGCAGAT 2790
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Db 2791 GGGGGCAAGTGCCCATCAAGTGGATGGCGTGGAGTCCATTTCTCCCGCGGCTTCAAC 2850
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QY 653 ----- 653
Db 2971 CTGCCCCAGCCCCCATCTGCACCATGTGTCTACATGATCATGTGTCAAATGTTGGATG 3030
QY 653 ----- 653
Db 3031 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTTGGTGTCTGNAATTCCTCCGCATGGCC 3090
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3091 AGGGACCCCGCGCTTTGTGTCTATCCAGAAATGAGGACTTGGGCCCGCAGTCCCTTG 3150
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3151 GACAGCACCTTCTACCGCTCCTGCTGGAGGAGATGACATGGGGGACCTGGTGGATGCT 3210
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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QY 705 GlyMetValHisArgHisArg 712
Db 3271 GGCATGGTCCACCACAGGCCCGC 3294
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RESULT 11

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US-09-527-487-1
; Sequence 1, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(3915)
US-09-527-487-1
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Alignment Scores:

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Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1
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US-09-493-480-7 (1-712) x US-09-527-487-1 (1-4530)

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QY 1 MetGluLeuAlaAlaLeuCysArgTTPGlyLeuLeuAlaLeuProGlyAla 20
Db 151 ATGGAGCTGGCGGCTTGTGCCCTGGGGCTCTCTCTCGCCCTCTTTCGCCCGGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCAGAGCAACCAAGTGTGCACCGGCACAGACATGAAGCTGGGGCTCCCTGCGAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 271 ACCCAGCTGGACATGTCTCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGGAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 331 GAACTCACCTTACCTGGCCCAATGCCAGCCTGTCTCTCTGCGAGGATATCCAGGAGGTG 390
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGTACGTGTCTATCGCTCAACCAAGTGCAGGAGGTCCCTGCTGCAGAGGCTCGGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAspTyrAlaLeuAlaValLeuAspAsnGly 120
Db 451 ATTGTGCGAGGCCACCCAGCTCTTTGAGGACCAATATGATGCCCTGCGCGTGTAGACAAATGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
Db 511 GACCCCTGAAACAATAACACCCCTGTCCAGAGGGGCTTCCCGAGGAGGCTCGCGGAGCTG 570
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 571 CAGCTTCGAAGCCTCAGAGATCTTGNAAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 631 CTCTGCTACCCAGGACACGATTTTGTGGAGGACATCTTCCACAAGAACCAACAGCTGGCT 690
QY 181 LeuThrIleLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 691 CTCACACTGATAGACCAACCCGCTCTCGGGGCTTGCACCCCTGTCTTCTCCGATGTGTAAG 750
QY 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 751 GGCTCCCGCTGCTGGGGAGAGATTTCTGAGGATTTGTAGAGCCTGACAGCCCTGCTGTCTGT 810
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 811 GCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProlLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 871 GCTGCGGGCTGCACGGGGCCCAAGCACTCTGACTGCTGGCTGCGCTGCCCTCCACTTCAACAC 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 931 AGTGGCATCTGTGAGCTGCACCTGCCCGCCCTGGTCACTACCAACACAGACAGATTTGAG 990
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 991 TCCATGCCCAATCCCGAGGGCGGTATACATTCCGGGCCAGCTGTGTGACTGCTGCTGCC 1050
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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Db	1051	TACAACTACCTTTCTACGACGTGGGATCTCTGCACCCCTGCTCTGCCCCCTGCACACCAA	1110	QY	653	-----	653
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	Db	2191	AGATCCGGAAGTACACGATCGGAGACTGTCTGCAGGAAACGGAGCTGTGTGGAGCCGCTG	2250
Db	1111	GAGGTACAGCAGAGAGATGGAAACACAGCCGTGTGGAAGTGCAGAGCCCTGTGCCCCGA	1170	QY	653	-----	653
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	Db	2251	ACACCTAGCGGAGCGATGCCAACCAAGCGGAGATGCGGATCCTGAAAGAGACGGAGCTG	2310
Db	1171	GTGTGCTATGGTCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACCAAGTGCCAAT	1230	QY	653	-----	653
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	Db	2311	AGGAAGGTGAAGTGTCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC	2370
Db	1231	ATCCAGAGATTTGCTGGCTGCAAGAGATCTTTGGGAGCTGGCAATTTCTGCCGAGAGC	1290	QY	653	-----	653
QY	381	PheAspGlyAspProAlaSerIleThrAlaProLeuGlnProGluGlnLeuValPhe	400	Db	2371	CCTGATGGGGAATGTGAAAATTCAGTGGCCATCAAAGTGTGAGGAAAAACACATCC	2430
Db	1291	TTTGATGGGACCCAGCCCTCCAACTGCCCGCTCCAGCAGAGCAGCTCCAAGTGTTT	1350	QY	653	-----	653
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	Db	2431	CCCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGCTCCCCA	2490
Db	1351	GAGACTCTGGAAGAGATCACAGTTACCTATATACATCTCAGCATGGCGGACAGCCTGCCT	1410	QY	653	-----	653
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	Db	2491	TATGTCTCCGCTTCTTGGGCATCTGCCTGACATCCAAGTGCAGCTGGTGTGACACAGCTT	2550
Db	1411	GACCTCAGCGTCTTCAGAACCTGCAAGTAATCCGGGAGCAATTCCTGCACAATGGCGCC	1470	QY	653	-----	653
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460	Db	2551	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGAGCCCTGGGCTCCCAG	2610
Db	1471	TACTCTGACCTCGACGGCTTGGGCATCAGCTGGCTGGGCTGGCTCACTGAGGGAA	1530	QY	653	-----	653
QY	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480	Db	2611	GACCTGTCTGAACACTGGTGTATGCAGATTGCCAAGGGGATGAGTACTCTGGAGGATGTGCG	2670
Db	1531	CTGGCAGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTCTGTCACACGGTG	1590	QY	653	-----	653
QY	481	ProTrpAspGlnLeuPheArgIleProHisGlnAlaLeuLeuHisThrAlaIleArgPro	500	Db	2671	CTCGTACACAGGGAATTTGGCCGCTCGGAACGTGTGTGTCAGAGTCCCAACCATGTCAAA	2730
Db	1591	CCCTGGGACAGCTCTTTCCGAACCCGCAACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1650	QY	653	-----	653
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	Db	2731	ATTACAGACTTCGGGCTGGCTGGCTGGTGGACATTGACGACACAGAGTACCATGCAGAT	2790
Db	1651	GAGGACAGTGTGTGGCCGAGGCGCTTGGCTCGCCACAGCTGTGGCCCGGAGGCACTGC	1710	QY	653	-----	653
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	Db	2791	GGGGCAAAGTGCCTCATCAAGTGGATGGCTGGCTGGAGTCCATTCTCCGCGCGGTTTCCAC	2850
Db	1711	TGGGTCCAGGCCCCACCCAGTGTGTCAACTGCAGCCAGTCTCTTCGGGGCCAGAGTGC	1770	QY	653	-----	653
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	Db	2851	CACCAGATGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC	2910
Db	1771	GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCAGGGAGTATGTGAATGCCAGGCATGT	1830	QY	653	-----	653
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	Db	2911	AAACCTTACGATGGGATCCAGCCCCGGAGATCCCTGACCTGCTGAAAAAGGGAGCGG	2970
Db	1831	TTGCCGTGCACCTGAGTGTGAGCCCCAGAAATGGCTCAGTACCTGTTTTTGACCGGAG	1890	QY	653	-----	653
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600	Db	2971	CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAATGTTGGATG	3030
Db	1891	GCTGACCAAGTGTGGCCTGTGCCACTATAGGACCTCCCTTCTGCGTGGCCCGCTGC	1950	QY	653	-----	653
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620	Db	3031	ATTGACTCTGAATGTCGCCAAGATTCCGGGAGTTGGTGTCTGAAATTTCTCCCGCATGGCC	3090
Db	1951	CCGAGCGGTGTGAACCTGACCTCTCTACATGCCCCATCTGGAAGTTTCCAGATGAGGAG	2010	QY	654	-----	664
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys	640	Db	3091	AGGGACCCCGAGCGCTTTGTGTCATCCAGATGAGGACTTGGGCCACCGCAGTCCCTTG	3150
Db	2011	GGCGCATGCCAGCTTGGCCCATCAACTGCACCCACTCTCTGTGTGACCTGGATGACAAG	2070	QY	665	AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653	Db	3151	GACAGCACCTTCTACCGCTCACTGTGGAGGACGATGACATGGGGACCTGTGTGATGTCT	3210
Db	2071	GGCTGCCCGCGAGCAGAGACGACCCCTCTGACGTCCATCTGCTCTCGCGGTGTGGC	2130	QY	685	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	704
QY	653	-----	653	Db	3211	GAGGAGTATCTGGTACCACCGCAGCAGGGCTTCTTCTGTCCAGACCCCTGCCCGGGCGCTGG	3270
Db	2131	ATTCTGCTGGTCTGTGGGTGTGGTCTTTTGGGATCCTCATCAAGCGCAGCGGAGCAG	2190				

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QY 705 GlyMetValHisHisArgHisArg 712
Db 3271 GGCATGGTCCACCACAGCCCGC 3294

RESULT 12
US-09-877-177A-11
; Sequence 11, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-11

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-7 (1-712) x US-09-877-177A-11 (1-4530)
QY 1 MetGluLeuAlaLeuCysArgTrrpGlyLeuLeuAlaLeuProGlyAla 20
Db 151 ATGAGCTGGCGGCTTGTGCGGCTGGGGGCTCTCTCTGCCCTCTTGGCCCCCGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCGAGCACCCAGTGTGCACCGGCACAGACATGNAGCTGGGGCTCTCTGCGAGTCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 271 ACCACCTGGACATGCTCCGCCACCTTACACGGGCTGCCAGGTGGTGGAGGAAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 331 GAACCTACCTACCTGCCCAATGCCAGGCTGTCTCTCTGAGGATATCCAGGAGGTG 390
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGCTACGTGCTCATCGCTCACACCAAGTGGGAGGTGCCACTGCAGAGGCTGGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 451 ATTGTGCGAGGCCACCAAGCTCTTTAGGACAACTATGCCCTCGCGGTGTAGACAAATGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 511 GACCCGCTGAACAATACACCCCTGTCCAGGGGCTCTCCAGAGGCGCTTGGGGAGCTG 570
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 571 CAGCTTCGAAGCTTCACAGAGATCTTGAAGAGGGGTCTTGTATCCAGCGGAAACCCCG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTrrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 631 CTCTGCTACAGGACACGATTTTGTGGAAGGACATCTTCCACAAAGAACCAACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisAspProMetCysLys 200
Db 691 CTCACACTGATAGACACCAACCCGCTCTCGGGCTTGCACCCCTGTCTTCCGATGTGTAAG 750

201 GlySerArgCysTrrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
751 GGCTCCCGCTGCTGGGGAGAGATTCTGAGGATTGTGAGAGCTGTGACGCGCTGCTGTCTGT 810
221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
811 GCGGTGGGCTGTGCCCGCTGCAGAGGGGCCACTGCCACTGCTGCTGCCATGAGCAGTGT 870
241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
871 GCTGCCGGCTGCACGGGCCCCAGCACTCTGACTGCTGCTGCCCTGCTTCCACTTCAACCAC 930
261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
931 AGTGGCATCTGTGAGCTGCACCTGCCAGGCCCTGGTCACTACCAACACAGACAGCTTTGAG 990
281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
991 TCCATGCCCAATCCCGAGGGCCGGTATACATTCCGGGCCAGCTGTGTGACTGTGCTGTCCC 1050
301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
1051 TACAACTACTTCTACGGACGTGGGATCTGTGACCTCTGCTGCCCTTGCACCAACCAA 1110
321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
1111 GAGGTGCACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA 1170
341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
1171 GTGTGCTATGTCTGGGCATGGAGCACTTGCAGAGGTGAGGCGCATACAGTGCCTCAAT 1230
361 IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
1231 ATCCAGAGTGTGCTGGCTGCAGAGAGATCTTTGGAGGCTGCGATTTCTTCCGGAGAGC 1290
381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
1291 TTTGATGGGGACCCAGCCCTCCAACACTGCCCCGCTCCAGCCAGCAGCAGCTCCAAGTGT 1350
401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrrpProAspSerLeuPro 420
1351 GAGACTCTGGAAGAGATCAAGGTTTACCTATATACATCTCAGCATGGCGGAGCAGCTGCCT 1410
421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
1411 GACCTCAGGCTCTTCCAGAACCTGCAAGTAATCCGGGGAGCAATTTCTGCACATGGGCCC 1470
441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrrpLeuGlyLeuArgSerLeuArgGlu 460
1471 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGGAA 1530
461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
1531 CTGGGAGTGGACTGGCCCTCATCCACCAATAACACCCACTCTGCTTCTGTCGACACCGGTG 1590
481 ProTrrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
1591 CCTGGGACACAGCTCTTTGGAAACCCGACCAAGCTTGTGCTCCACACTGCCAACCGGCCA 1650
501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
1651 GAGGACAGTGTGTGGGCGGAGGCGCTTGGCTGCCACAGCTGTGCTGCCCGCGGAGGCACTGC 1710
521 TrrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGlnCys 540
1711 TGGGGTTCAGGGGCCCAACCCAGTGTGTCAACTGCAGCAGTTCCTTCCGGGCGAGGAGTGC 1770
541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
1771 GTGGAGGAATGCCAGTACTTGCAGGGGCTTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1830
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QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1831 TTGCCGTGCCACCTGAGTGTAGCCCCCAGAGATGGCTAGTACCTGTTTGGACCGGAG 1890
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 1891 GCTGACCAAGTGTGGCCTGTGCCACTATAAGGACCTCCCTTCTGCGTCCCGCTGC 1950
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrPheProAspGluGlu 620
Db 1951 CCACGGGTGTAAACCTGACCTCTCTATACATGCCCATCTGGAAGTTTCCAGATAGGAG 2010
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db 2011 GCGCATGCGAGCCTTGCCCCATCACTGCACCCACTCTCTGTGGACCTGATGACAG 2070
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 2071 GGCTGCCCGCGAGCAGAGACGACGCCCTCTGCACGTCCATCGTCTCTCGGTGGTTGC 2130
QY 653 ----- 653
Db 2131 ATTCTGCTGTCGTGTCCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGACAG 2190
QY 653 ----- 653
Db 2191 AAGATCCGGNAGTACACGATCGGAGACTGCTCAGGAAACGGAGCTGTTGGACCGCTG 2250
QY 653 ----- 653
Db 2251 ACACCTAGCGGAGCGATGCCAACCAAGCGGCAGATCGGATCCTGAAAGACGAGCTG 2310
QY 653 ----- 653
Db 2311 AGAAGGTGAAGTGTCTGGATCTGGCTTTGGCACAGTCTCAAGGGCATCTGGATC 2370
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Db 2371 CCTGATGGGGAGATGTGAAATTCAGTGGCCATCAAGTGTGAGGAAACACATCC 2430
QY 653 ----- 653
Db 2431 CCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGCTGTTGGCTCCCA 2490
QY 653 ----- 653
Db 2491 TATGTCCTCCGCTTCTGGGCATCTGCCCTGACATCCACGGTGAGCTGTGACACAGCTT 2550
QY 653 ----- 653
Db 2551 ATGCCCTATGGCTCCTTAGACCATGTCCGGRAAACCGCGAGCCCTGGCTCCCA 2610
QY 653 ----- 653
Db 2611 GACCTGCTGAAGTGTGTATGACATTTGCCAAGGGATGAGTACCTGGAGGATGTCGG 2670
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Db 2671 CTCGTACACAGGACTTGGCCGCTCGGAACGTGCTCGGTCAGAGTCCCAACCATGTCAA 2730
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Db 2731 ATTACAGACTTCGGGTGGCTCGGCTGCTGGACATTGACGACAGAGTACCATGCAGAT 2790
QY 653 ----- 653
Db 2791 GGCGGCAAGGTGCCCCATCAAGTGGATGGCGTGGAGTCCATTCTCCGCGGGGTTTACC 2850
QY 653 ----- 653
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Db 2911 AAACCTTAGATGGATCCACGCCGGGAGATCCCTGACCTGCTGAAAAAGGGGAGCG 2970
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Db 2971 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTATCATGATCATGTCAAATGTTGGATG 3030
QY 653 ----- 653
Db 3031 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC 3090
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3091 AGGGACCCCCAGCGCTTTGTGTGTCATCCAGAATGAGGACTTGGGCCCCAGCCAGTCCCTTG 3150
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3151 GACAGACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT 3210
QY 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
Db 3211 GAGGAGTATCTGTACCCAGCAGGCTTCTTCTGTCAAGACCTGCCCGGCGCTGG 3270
QY 705 GlyMetValHisHisArgHisarg 712
Db 3271 GGCATGGTCCACCACACGACCGCGC 3294
RESULT 13
US-09-811-115-1
; Sequence 1, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector Sequence
US-09-811-115-1
Alignment Scores:
Pred. No.: 0 Length: 9274
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1
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QY 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 1731 ATGGAGCTGGCGCCCTTGTGCGCTGGGGCTCTCTCTCGCCCTTGTGCCCGGAGCC 1790
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 1791 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGTGCAGTCCCTGCCAGTCCCGAG 1850
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 1851 ACCCACCTGGACATGCTCCGCCACCTCTTACCAGGGCTGCCAGGTGTGTCAGGGAACCTG 1910
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Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 1911 GAACCTCACTACCTGCCCCACCAATGCCAGCGCTGCTTCTTCCAGGATATCCAGAGAGTG 1970
Qy 81 GlnGlyTyrValLeuLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 1971 CAGGGCTACGTGCTCATCGCTCACAAACAGTAGGAGAGGTCCACCTGCAGAGAGCTGGG 2030
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 2031 ATTGTGGAGGACCCAGCTCTTTTGGAGCAACTATGCTCCCTGGCGGTAGACAAATGGA 2090
Qy 121 AspProLeuAsnAsnThrThrProValThrClyAlaSerProGlyGlyLeuArgGluLeu 140
Db 2091 GACCCGCTGAACAATACACCCCTGTACAGGGGCTTCCAGAGAGGCTGCGGGAGCTG 2150
Qy 141 GlnLeuArgSerLeuThrGluLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 2151 CAGCTTCGAAGCTTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCCOAG 2210
Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 2211 CTCTGCTACCAAGACACGATTTTGTGAAGGACATCTTCCACAAGAAACACACAGCTGGCT 2270
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 2271 CTCACACTGATAGACACCAACCGCTCTCGGGCTTCCACCCCTGTTCTCCGATGTGAAG 2330
Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 2331 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGGATTTGTAGAGCTTCAGAGCCTGACGGCAGCTGTCTGT 2390
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 2391 GCCGGTGGCTGTGCCCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 2450
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 2451 GCTGCCGGCTGCACGGGCCCAACAGCACTCTGACTGCCCTGGCTGCCCTCCACTTCAACAC 2510
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 2511 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTGTACCTACAAACACAGACAGCTTTGAG 2570
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 2571 TCCATGCCCAATCCGAGGGCCGTATACATTCCGGCCAGCTGTGTGACTGCTGCTCCC 2630
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 2631 TACAACCTACCTTTCTAGCGAGCTGGGATCTCTGCACCCCTCGTCTGCCCCCTGCACAAACAA 2690
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 2691 GAGGTGACAGAGGATGAAACACAGCGGTGTGAGAAGTGCAGAAAGCCCTGTGGCCGA 2750
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 2751 GTGTGCTATGCTCTGGCATGGAGCACTTCGAGAGGTGAGGGCAGTTACAGTGGCCAAAT 2810
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 2811 ATCCAGAGATTGTGGCTGCAGAAGATCTTTGGGAGCCTGGCAATTTCTGCCGGAGAGC 2870
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 2871 TTTGATGGGACCCAGGCTCCAAACACTGCCCGCTCCAGCCAGAGCAGCTCCCAAGTGT 2930
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 2931 GAGACTCTGGAGAGATCACAGGTTACTATACATCTCAGCATGGCCGGACAGCTGCT 2990
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440

Db 2991 GACCTCAGCGCTCTTCCAGAACCTTGCAGAGTAATCCGGGGAGCAATTTCTGCAAAATGGCGCC 3050
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 3051 TACTCGCTGACCTTGCNAAGGCTGGGCATCAGCTGGCTGGGGCTGCCCTCTACTGAGGGAA 3110
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
Db 3111 CTGGCAGTGGACTGGCCCTCATCCACATAAACACCCACCTCTGCTTCTGTCACACAGCTG 3170
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 3171 CCCTGGGACAGCTCTTTTGGAAACCCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA 3230
Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 3231 GAGGACAGTGTGTGGCGAGGGCTGGCCCTGCCACAGCTGTGGGCCCGGAGGCACTGC 3290
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 3291 TGGGTCCAGGGCCCAACCCAGTGTGTCAACTGCAGCCAGTTCTTCTCGGGCCAGGAGTGC 3350
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 3351 GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGAGATGTGAAATGCCAGGCACTGT 3410
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 3411 TTGCCGTGCCACCTGANGTGTAGCCCCAGAAATGGCTCAGTGACTGTCTTTGGACCGGAG 3470
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 3471 GCTGACCCAGTGTGGCTGTGCCACTATAAGGACCTCCCTTCTGCGTGGCCCGCTGC 3530
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
Db 3531 CCAGCGGTGTGAACCTGACCTCTCTACATGCCATCTCGAAGATTTTCCAGATGAGGAG 3590
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 3591 GGGCATGCCAGCTTGGCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAG 3650
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 3651 GGCTGCCCGCCGAGCAGAGAGAGCCCTCTGACGTCCTCGTCTCTGCGGTGGTTGGC 3710
Qy 653 ----- 653
Db 3711 ATTTCTGCTGCTGCTTGTGGGGTGGTCTTTTGGGATCTCTATCAAGCGACGCGCAG 3770
Qy 653 ----- 653
Db 3771 AAGATCCGGNAGTACAGATGCCGAGACTGCTGCAGGAAACGGAGCTGTGGAGCCCGCTG 3830
Qy 653 ----- 653
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Qy 653 ----- 653
Db 3891 AGGAAGGTGAAGGTGCTTGGATCTGGGCTTTTGGCAGCTCTACAAGGGCATCTGGATC 3950
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Db 3951 CCTGATGGGGAGAAATGTGAAAATTTCCAGTGGCCCATCAAAGTGTGTAGGGAAAAACACATCC 4010
Qy 653 ----- 653
Db 4011 CCCAAAGCCAAACAAAGAAATCTTTAGAGAGCATACGTGATGCTGTGTGGGTCCCCCA 4070
Qy 653 ----- 653

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Db 4071 TATGTCTCCGCTTCTGGCATCTGCTGCATCCACGGTGAGCTGGTGACACAGCTT 4130
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Db 4131 ATGCCCTATGTGCTCTTTAGACCATGTCCGGGAAACCGCGAGCCTGGGCTCCAG 4190
QY 653 -----
Db 4191 GACCTGCTGAATCTGGTGTATGAGATTGCCAAGGGGATGAGTACTCTGGAGGATGGCG 4250
QY 653 -----
Db 4251 CTCGTACACAGGAGCTTGGCCGCTCGAAGCTGCTGGTCAAGAGTCCCAACCATGTCAA 4310
QY 653 -----
Db 4311 ATTACAGACTTCCGGCTGCTGGCTGGTGGACATTGACAGAGTACCATGCAGAT 4370
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Db 4371 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGCGGTTCCAC 4430
QY 653 -----
Db 4431 CACCAGAGTATGTGTGAGATTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 4490
QY 653 -----
Db 4491 AAACCTTACATGGGATCCAGCCCGGAGATCCCTGACCTGCTGTAAGAAAGGGGAGCGG 4550
QY 653 -----
Db 4551 CTGCCCCAGCCCCCATCTGCACCATTTGATGTATCATGATCATGTGCTCAATGTTGGATG 4610
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Db 4611 ATTGACTCTGAATGTCCGCCAAGATTCCGGGAGTTGGTGTCTGAATTTCCCGCATGGCC 4670
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 4671 AGGACCCCGCAGGCTTTGTGTGTCATCCAGAATGAGGACTTGGGCCACCCAGTCCCTTG 4730
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 4731 GACAGACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGGTGATGCT 4790
QY 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
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Db 4851 GGATGTGTCACACACAGGCACCGC 4874

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RESULT 14
US-09-146-283-3
; Sequence 3, Application US/09146283
; Patent No. 5976546
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8
; US-09-146-283-3

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Alignment Scores:
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Score: 3632.00 Matches: 659
Percent Similarity: 98.65% Conservative: 0
Best Local Similarity: 98.65% Mismatches: 5
Query Match: 91.86% Indels: 4
DB: 2 Gaps: 2

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US-09-493-480-7 (1-712) x US-09-146-283-3 (1-2385)

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; Sequence 3, Application US/08579823A
; Patent No. 6080409
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Composition and Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,823A
; FILING DATE: 03-DEC-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8

US-08-579-823A-3

Alignment Scores:

Pred. No.: 0 Length: 2385
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 Best Local Similarity: 98.65% Mismatches: 5
 Query Match: 91.86% Indels: 4
 DB: 3 Gaps: 2

US-09-493-480-7 (1-712) x US-08-579-823A-3 (1-2385)

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QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
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QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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5	3776	95.5	3768	9	US-09-854-356-9
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23	3776	95.5	4530	17	US-10-116-273-131
24	3776	95.5	4530	17	US-10-426-836-11
25	3776	95.5	4530	17	US-10-272-437A-27
26	3776	95.5	4530	17	US-10-117-937-595
27	3776	95.5	4530	17	US-10-392-113-45
28	3776	95.5	4530	17	US-10-159-563-208
29	3776	95.5	4530	17	US-10-435-696-10
30	3776	95.5	4530	19	US-10-734-564-59
31	3776	95.5	4530	19	US-10-657-022-91
32	3776	95.5	4530	21	US-10-615-343-16
33	3776	95.5	4530	21	US-10-928-465-75
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35	3776	95.5	4530	21	US-10-871-708-18
36	3776	95.5	4530	24	US-11-067-064-595
37	3776	95.5	4642	14	US-10-198-846-10896
38	3776	95.5	9274	9	US-09-811-123-7
39	3776	95.5	9274	9	US-09-811-115-1
40	3756	95.0	4606	10	US-09-971-392-70
41	3746.5	94.8	4647	22	US-10-956-373-9
42	3733	94.4	4543	9	US-09-769-508-1
43	3604	91.1	2320	22	US-10-956-373-1
44	3598.5	91.0	2164	17	US-10-412-804A-5
45	3595	90.9	2149	17	US-10-412-804A-9

ALIGNMENTS

RESULT 1

US-10-207-498-5
; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND HER3
; FILE REFERENCE: 30448.103-US-U1
; CURRENT APPLICATION NUMBER: US/10/207,498
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27

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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-207-498-5

Alignment Scores:
Pred. No.: 0 Length: 3765
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 15 Gaps: 1

US-09-493-480-7 (1-712) x US-10-207-498-5 (1-3765)

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DB 1 ATGGAGCTGGCGGCTTGTGCGCGCTGGGGCTCTCTCGCCCTCTTGGCCCCCGAGGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 61 GCGAGCACCAAGTGTGCACCGGCACAGACATGAGCTGCGGCTCTCTGCCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrgingGlyCysGlnValValGingGlyAsnLeu 60
DB 121 ACCCACCTGGACATGCTCGCCACCTCTACCAAGGCTGCGAGTGTGGTGTGCGGAGAACCTG 180
QY 61 GluLeuThrTyrlProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 181 GAACTCACCTAGCTGCCCAACCAATGCCAGCTGTCTCTCTGCGAGGATATCCAGAGGTG 240
QY 81 GlnGlyTyrlValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 241 CAGGGCTAGCTGCTCATCGCTCACACCAAGTGGAGGAGTCCCATCTGAGAGGTGGGG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrlAlaLeuAlaValLeuAspAsnGly 120
DB 301 ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCTGCTGCTGCTGCTGCTGCTG 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 361 GACCCGCTGAACAATACCAACCCCTGTTCAGGGGCTCTCCAGAGGCTGCGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValValLeuIleGlnArgAsnProGln 160
DB 421 CAGCTTCGAGGCTCACAGAGATCTTGAAGAGGGGGTCTTGATCCAGCGGAACCCCGAG 480
QY 161 LeuCysTyrlGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla 180
DB 481 CTCGTCTACAGACACAGATTTTGTGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAA 600
QY 201 GlySerArgCysTrpGlyGluSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 601 GGCTCCCGCTGTGGGAGAGATCTGAGGATTTGTAGAGCTGTGAGGCTGTGCTGTCTGT 660
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
DB 661 GCGGCTGGCTGTGCGCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCCATGAGCAGTGT 720
QY 241 AlaAlaGlyCysThrClyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 721 GCTGCGGCTGACGCGGCCCAAGCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
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QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrlAsnThrAspThrPheGlu 280
DB 781 AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTACAAACACACACACAGTTTGAG 840
QY 281 SerMetProAsnProGluGlyArgTyrlThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 841 TCCATGCCCAATCCCGAGGGCGGTATACATTTCCGGCGCCAGCTGTGTGACTGCCTGTGCC 900
QY 301 TyrAsnTyrlLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisGlnGln 320
DB 901 TACAACTACCTTTCTACGAGCTGGGATCCTGCACCCCTGCTGCCCCCTGCACAAACCAA 960
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 961 GAGGTGACAGCAGAGATGGAACACACAGCGGTGTGAGAGTGCAGACAGCCCTGTGCCCGA 1020
QY 341 ValCysTyrlGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1021 GTGTGCTATGCTGTGGGCATGGAGCACTTGGAGAGGTGAGGGCAGTTTACCAGTGCCTAT 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1081 ATCCAGGAGTTTGTGCTGCAAGAGATCTTTGGGAGCTTGGCATTTCTGCCGGAGAGC 1140
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1141 TTTGATGGGGACCCAGCCCTCCAACACTGCCCGCTCCAGCCAGCAGCAGCTCCAAGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrlLeuTyrlIleSerAlaTrpProAspSerLeuPro 420
DB 1201 GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGTGCGCGACAGCTGCCT 1260
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisGlnGlyAla 440
DB 1261 GACCTCAGCGCTCTCCAGAACCTGCAAGTAATCCGGGGAGCAATTTCTGCACAAATGGCGC 1320
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1321 TACTCGCTGACCTGCAAGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGGAA 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisIleAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGCAGTGGACTGGCCCTCATCCACCATTAACACCCACTCTGCTTGTGTGCACACGGTG 1440
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCCTGGGACAGCTCTTTCCGGAACCCGACCCAGCTCTGCTCCACACTGCCAACCGGCCA 1500
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACGAGTGTGTGGCGAGGGCTGGCCCTGCCACCACTGCTGCGCCGAGGGCACTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGCTCCAGGCGCCACCCAGCTGTCTCACTGCAGCCAGTTCTCTTCCGGGGCCAGGAGT 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrlValAsnAlaArgHisCys 560
DB 1621 GTGGAGGAATCCCGAGTACTGCGAGGGCTTCCCGAGGAGATGTGATGCCAGGCACTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1681 TTGCGCTGCCACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1740
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrlLysAspProPheCysValAlaArgCys 600
DB 1741 GCTGACCAAGTGTGGCTGTGCCACTATTAAGSACCTCTCCCTTGTGCGTGGCGCTGCTG 1800
QY 601 ProSerGlyValLysProAspLeuSerTyrlMetProIleTrpLysPheProAspGluGlu 620
DB 1801 CCCAGCGTGTGAACACTGACCTCTCTACATGCCCTCTCTGGAAGTTTCCAGATGAGGAG 1860
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
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Db 1861 |GGCGATGCCAGCCTTGCCCACTCAACTGCACCACTCTGTGTGGACCTGGATGCAAG 1920
Qy 641 |GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 |GGCTGCCCGCCGAGCAGAGCCAGCCCTCTGACGTCCATCTCTCTGCGGTGGTGGC 1980
Qy 653 |----- 653
Db 1981 |ATTCTGCTGCTGCTGTGCTTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCGCAG 2040
Qy 653 |----- 653
Db 2041 |AGATCCGGAAGTACAGATGCGGAGACTGTCGAGGAAACGGAGTGTGGAGCCGCTG 2100
Qy 653 |----- 653
Db 2101 |ACACTAGCGGAGGATGCCCAACAGCGCAGATCGGATCCTGAAAGAGAGCGAGCTG 2160
Qy 653 |----- 653
Db 2161 |AGGAAGTGAAGTGTCTTGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220
Qy 653 |----- 653
Db 2221 |CTGTATGGGGAGAAATGTGAAAATTCAGTGGCCATCAAAAGTGTGAGGGAAAAACATCC 2280
Qy 653 |----- 653
Db 2281 |CCCAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGCTGTGTGGGCTCCCCA 2340
Qy 653 |----- 653
Db 2341 |TATGTCTCCGCTTCTGGGCATCTGCTTGACATCCACGGTGCAGCTGGTGACACAGCTT 2400
Qy 653 |----- 653
Db 2401 |ATGCCCTATGGTGCCTCTTAGACCATGTCCGGGAAAAACCGCGAGCGCTGGGCTCCAG 2460
Qy 653 |----- 653
Db 2461 |GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGATGAGCTACCTGGAGGATGTCCG 2520
Qy 653 |----- 653
Db 2521 |CTGTACACAGGACTTGGCGCTCGGAACGTGCTGTCAGAGTCCCAACCATGTCAAA 2580
Qy 653 |----- 653
Db 2581 |ATTACAGACTTGGGGTGGCTCGGCTGTGGACATTGACGAGACAGATACCATGCAGAT 2640
Qy 653 |----- 653
Db 2641 |GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCGCGCGCGGTTCAAC 2700
Qy 653 |----- 653
Db 2701 |CACCAGAGTGATGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
Qy 653 |----- 653
Db 2761 |AAACCTTACATGGGATCCAGCCCGGAGATCCCTGACCTGTGGAAAAAGGGGAGCGG 2820
Qy 653 |----- 653
Db 2821 |CTGCCCGAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAATGTTGGATG 2880
Qy 653 |----- 653
Db 2881 |ATTGACTCTGAATGTCGGCCAGAGATCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
Qy 654 |-----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
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Db 2941 |AGGGACCCCGAGCGCTTTGTGTGTCATCCAGAAATGAGACTTGGGCCCGCAGTCCCTTG 3000
Qy 665 |AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
|-----|
Db 3001 |GACAGCACCTTCTTACCGCTCACTGCTGGAGGACGATGACATGGGACCTTGGTGGATGCT 3060
Qy 685 |GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
|-----|
Db 3061 |GAGGAGTATCTGTTACCCAGCAGGCGCTTCTTCTGTCCAGACCTGCCCCGGCGCTGGG 3120
Qy 705 |GlyMetValHisHisArgHisArg 712
|-----|
Db 3121 |GGCATGTTCCACCACAGGACCCGC 3144

RESULT 2
US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-erbB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-811-123-8

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 9 Gaps: 1

US-09-493-480-7 (1-712) x US-09-811-123-8 (1-3768)
Qy 1 |MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 1 |ATGGAGCTGGCGCCTTGTGCGCTGGGGCTCTCTCTGCGCCTTGTGCCCGCGAGCC 60
Qy 21 |AlaSerThrGlnValCysThrGlyThrAspMetLeuLeuArgLeuProAlaSerProGlu 40
Db 61 |GCGAGCACCAAGTGTGCACCGCACAGACATGAAGCTGCGGCTCCCTGTCAGTCCCGAG 120
Qy 41 |ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 |ACCCACTGGACATGCTCGCCACCTCTTACAGGGCTGCCAGGTGTGCAGGGAACCTG 180
Qy 61 |GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 |GAACTCACCTACTGCGCCCAACCAATGCCAGCTGTCTCTTCTGCGAGATATCCAGGAGTG 240
Qy 81 |GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 |CAGGGCTAGCTGCTCATCGCTCACACCAAGTGAGGAGGTCCCTACTGCAGAGGCTCGCG 300
Qy 101 |IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 |ATTGTGCGAGGACCCCGACCTCTTTGAGGACAACTATGCTGCGCTGCTGTAGCAATGGA 360
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121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
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141 GlnLeuArgSerLeuThrGluLeuLeuGlyGlyValLeuIleGlnArgAsnProGln 160
142 |
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161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisAsnAsnGlnLeuAla 180
162 |
481 CTCGTGTACAGACACGATTTTGTGAAGGACATCTTCCAAAGAACCAACAGCTGGCT 540
181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
202 |
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221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
222 |
661 GCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCACCTGACTGTCTGCCATGAGCAGTGT 720
241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
242 |
721 GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGCTGGCTGCTCCCTCCACTTCAACCAAC 780
261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
281 |
781 AGTGGCATCTGTGAGCTGCACTGCCAGCGCTGGTCACCTACAAACACAGACACGTTTGAG 840
281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
282 |
841 TCCATGCCCAATCCCGAGGGCCGGTATACATTGGGGCCAGCTGTGTGACTGCCCTGTGCC 900
301 TyrAsnThrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
302 |
901 TACAACCTACTTCTACGGACGTGGATCTTGACCCCTGCTGTGCCCTGTCACAAACCAA 960
321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
322 |
961 GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA 1020
341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
342 |
1021 GTGTGCTATGTGTGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACCAAGTGCAT 1080
361 IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
381 |
1081 ATCCAGGAGTTTGTGGCTGCAAGAAGATCTTTGGGAGCTGGCATTTCTGCCGGAGAGC 1140
381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
382 |
1141 TTTGATGGGGACCCAGCCCTCAACACTGCCCGCTCCAGCCAGCAGCAGCTCCAAAGTGT 1200
401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
421 |
1201 GAGACTCTGGAGAGATCAGGTACCTATACATCTCAGCATGGCCGAGCAGCCTGGCT 1260
421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
441 |
1261 GACCTCAGCGCTTCTCCAGAACCTGCAAGTAATCCGGGAGCAATTTCTGCACAAATGGCGC 1320
441 TyrSerLeuThrLeuGlnGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
461 |
1321 TACTCGCTACCCCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCGCTCACTGAGGAA 1380
461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisCysPheValHisThrVal 480
481 |
1381 CTGGGCACTGAGTGGCCCTCATCCACCAATACACCCACTCTGTCTTCGTGCACACGGTG 1440
481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500

1441 CCCTGGGACCAAGCTCTTTCCGAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1500
501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
502 |
1501 GAGGACGAGTGTGTGGCGAGGGCCTGCTGCCACCAAGCTGTGGCCCGAGGGCACTGC 1560
521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
522 |
1561 TGGGTCCAGGGCCCAACAGTGTCAACTGCACCAAGTTCCTTCGGGGCCAGGAGTGC 1620
541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
542 |
1621 GTGGAGGAATCCGAGTACTGCAGGGCTCCCCAGGAGTATGTGAATGCCAGGCACCTGT 1680
561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
581 |
1681 TTGCCGTGCCACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1740
581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
582 |
1741 GCTGACCAAGTGTGGCTGTGCCACTATAGGACCTTCCCTTCTGCTGGTCCCGCTGC 1800
601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
602 |
1801 CCCACGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
641 |
1861 GCGCATGCCAGCTTGGCCCACTCAACTCACTCACTCACTCACTCACTCACTCACTCACTCA 1920
641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
1921 GGCTCCCCCGCAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTCGCGTGTGTGGC 1980
653 |
1981 ATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
653 |
2041 AAGATCCGGAAGTACACGATGCGGAGACTGTGTCAGGAAACGAGACTGTGTGAGCGCGTG 2100
653 |
2101 ACACCTAGCGGAGCGATGCCCAACCGAGCGCAGATGCGGATCCTGAAAGAGACGAGGCTG 2160
653 |
2161 AGGAAGGTGAAGTGTCTGGATCTGGCGCTTTGGCACAGTCTACAAGGGCATCTGGATC 2220
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2221 CCTGATGGGAGAAATGTGAAAATTCCAGTGGCCATCAAAAGTGTGAGGAAAACACATCC 2280
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2281 CCCAAGCCAAACAAGAAATCTTAGACGACGATACGTGATGGTGTGGGTCTCCCA 2340
653 |
2341 TATGTCTCCCGCTTCTGGGATCTGCTGACATCCACGCTGACATCCACGCTGCTGCTGACACAGCTT 2400
653 |
2401 ATGCCCTATGCTGCTCTTTAGACCATGTCCGGGAAAACCGCGGACGCTTGGGTCTCCCA 2460
653 |
2461 GACCTGCTGAAGTGTGTATGACAGATTGCCAAGGGGATGAGCTACTGAGGATGTGCGG 2520
653 |
2521 GACCTGCTGAAGTGTGTATGACAGATTGCCAAGGGGATGAGCTACTGAGGATGTGCGG 2580
653 |
2581 GACCTGCTGAAGTGTGTATGACAGATTGCCAAGGGGATGAGCTACTGAGGATGTGCGG 2640
653 |

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Db 2521 CTCGTACACAGGACTTGGCGGCTCGGAACGTGCTCAAGAGTCCCAACCATGTCAA 2580
QY 653 -----
Db 2581 ATTACAGACTTCGGGCTGGCTCGGCTGCTGGACATTGACGACAGAGTACCATGCAGAT 2640
QY 653 -----
Db 2641 GGGGCAAGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGCTTACC 2700
QY 653 -----
Db 2701 CACCAGATGATGTGGAGTTATGTGTGACTGTGTGGAGGCTGATGACTTTTGGGGCC 2760
QY 653 -----
Db 2761 AAACCTTACGATGGATCCCGAGCCCGGAGATCCCTGACCTGCTGGAAAGGGGAGCGG 2820
QY 653 -----
Db 2821 CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGTCAAATGTGGATG 2880
QY 653 -----
Db 2881 ATTGACTCTGAATGTGGGCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGAGCGCTTGTGGTCTATCCAGAAATGAGGACTTGGGCCCGAGCAGCTCCCTTG 3000
QY 665 AppSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGACACCTTCTACCCTGCTACCTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTATCCCGACAGGAGGCTTCTTGTCTCCAGACCTTGCCCGCGGCGCTGGG 3120
QY 705 GlyMetValHisArgHisArg 712
Db 3121 GGCATGGTCCACACAGGCACCGC 3144
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RESULT 3

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US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2
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Alignment Scores:

Prod. No.:	0	Length:	3768
Score:	3776.00	Matches:	712
Percent Similarity:	67.94%	Conservative:	0
Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
DB:	9	Gaps:	1

US-09-493-480-7 (1-712) x US-09-811-115-2 (1-3768)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
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QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
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QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
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QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
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QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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RESULT 4

US-09-765-973-1
; Sequence 1, Application US/09765973
; Publication No. US20020039573A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.

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 RESULT 5
 US-09-854-356-9
 ; Sequence 9, Application US/09854356
 ; Patent No. US20020177567A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Gheysen, Dirk
 ; APPLICANT: Corixa Corporation
 ; APPLICANT: SmithKline Beecham Biologicals S. A.
 ; TITLE OF INVENTION: HER-2/neu Fusion Proteins
 ; FILE REFERENCE: 014058-009810PC
 ; CURRENT APPLICATION NUMBER: US/09/854,356
 ; CURRENT FILING DATE: 2001-05-09
 ; PRIOR APPLICATION NUMBER: US 09/493,480
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 60/117,976
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
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 ; LOCATION: (1)..(1959)
 ; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
 ; NAME/KEY: misc_feature
 ; LOCATION: (202)..(3765)
 ; OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
 ; NAME/KEY: misc_feature
 ; LOCATION: (2968)..(3765)
 ; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
 ; NAME/KEY: misc_feature
 ; LOCATION: (296)..(3144)
 ; OTHER INFORMATION: preferred portion of the phosphorylation domain
 ; OTHER INFORMATION: (delta PD) of human HER-2/neu
 US-09-854-356-9
 Alignment Scores:
 Pred. No.: 0 Length: 3768
 Score: 3776.00 Matches: 712
 Percent Similarity: 67.94% Conservative: 0
 Best Local Similarity: 67.94% Mismatches: 0
 Query Match: 95.50% Indels: 336
 DB: 9 Gaps: 1
 US-09-493-480-7 (1-712) x US-09-854-356-9 (1-3768)
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QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTATCCCGCAGCAGGGCTTCTTCTGTCTCAGACCTTGCCTCCGCGCTGG 3120
QY 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGGTCCACACAGGACCGC 3144
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RESULT 6

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US-09-930-125-1
; Sequence 1, Application US/09930125
; Publication No. US2002019329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
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; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedwick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; FILE REFERENCE: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-930-125-1
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Alignment Scores:

Pred. No.:	0	Length:	3768
Score:	3776.00	Matches:	712
Percent Similarity:	67.94%	Conservative:	0
Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
DB:	9	Gaps:	1

US-09-493-480-7 (1-712) x US-09-930-125-1 (1-3768)

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QY 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 1 ATGGAGCTGGCGCTTGTGGCGTGGGGCTCTCTCTCGCCCTCTTGTCCCGGAGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAAGTGTGACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCCG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCCACTTGGACATGCTCGCCACCTCTACCAAGGCTGCCAGGTGGTGCAGGGAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACCTCACCTACCTGCCCAACCAATGCCAGCTGTCTCTCTCCAGGATATCCAGGAGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTACGTGCTCATCGCTCACAAACCAAGTGAGGCAAGTCCCACTGCAGAGGTGCG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTACACATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAAATACACACCCCTGTCAAGGGGCTCCCAAGGAGGCTCGCGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyIleValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCTCACAGAGATCTTGAAGAGAGGGGTCTTGATCCAGCGGAACCCCC 480
QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACCAGGACACGATTTTGTGGAAGGACATCTTCCACAGACCAACAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGAAG 600
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGGATTTCTAGAGCTGTGACGCGCACTGTCTGT 660
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QY 221 AlaGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
DB 661 GCCGGTGGCTGTGCCCTGCAAGGGGCCACTGCCACTGACTGCTGCCACTGACAGTGT 720
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 721 GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGCTGCCCTGCCCTCCACTTCAACCA 780
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 781 AGTGGCATCTGTGAGCTGCATGCCACAGCCCTGGTCACTTACACACAGACACGTTTGA 840
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 841 TCCATGCCCAATCCGAGGGCCCGGTATACATTCGGCGCCAGCTGTGTGACTGCTGTCCC 900
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1021 GTGTGCTATGCTTGGCGCATGGAGCACTTCGAGAGGTGAGGCGAGTTACAGTGGCCA 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1081 ATCAGAGATTTGCTGCTGCACAGAAAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAG 1140
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
DB 1141 TTTGATGGGACCCAGCCTCCACACTGCCCGCTCCAGCCAGAGAGCTCCAGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
DB 1201 GAGACTCTGGAGAGATCACAGGTACCTATACATCTCAGCATGGCGGAGCAGCTGCCT 1260
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1261 GACCTCAGCGTCTTCAGAACCTGCAGATTAATCCGGGGAGCAATTTGCACAAATGGCGCC 1320
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1321 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTCAGGGAA 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGCAGTGAATGGCCCTCATCCACCAATAACACCCACCTCTGCTTCGTGCACACGGTG 1440
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCTTGGGACCAAGCTCTTTTCGGAACCCGACCAAGCTCTGCTCCACACTGCAACCGGCCA 1500
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACAGTGTGTGGCGAGGGCTTGGCCCTGGCCACAGCTGTGGCCCGAGGGCACTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGGTCCAGGGCCCAACCAAGTGTGTCACTGACGACAGTTCTTCGGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1621 GTGGAGGAATGCCAGGTACTGCAGGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1681 TTGCCGTGCCACCCTGAGTGTACAGCCCAAGATGGCTCAGTGCACCTTTTGGACCGGAG 1740

QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
DB 1741 GCTGACCCAGTGTGGCTGTGCCCACTATAAGACCCCTCCCTTCTCGTGGCCCGTGC 1800
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
DB 1801 CCAGGGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAAGTTTCCAGATGAGAG 1860
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
DB 1861 GCGCATGCCAGCCTTGGCCCATCACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG 1920
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
DB 1921 GGCTGCCCGCCGAGCAGAGAGCCCTCTGACGTCATCTCTCGCGGTGGTTGGC 1980
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DB 1981 ATTCTGTGTGCTGTGCTTTGGGGGTGGTCTTTGGGATCCTCATCAAGCCAGCGCAGAG 2040
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DB 2041 AAGATCCGGAAGTACAGATGCCGAGACTGCTGCAGAAACGGAGCTGGTGGAGCCGCTG 2100
QY 653 ----- 653
DB 2101 ACACCTAGCGAGCGATGCCAACACAGCGCAGATCGGATCCTTGAAAGAGACGGAGCTG 2160
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DB 2221 CCTGATGGGAGAAATCTGAAATTTCCAGTGGCCCATCAAAAGTTGTAGGGAAACACATCC 2280
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DB 2581 ATTACAGACTTCGGGCTGGCTCGGCTGTGGACATTTGACAGACAGAGTACCATGCAGAT 2640
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Db 2941 AGGGACCCCGAGGGCTTTGTGTGTCATCCAGAAATGAGACTTGGGCCCGACCCAGTCCCTTG 3000
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Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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Db 3121 GGCATGCTCCACACAGGACCGC 3144

RESULT 7
US-09-984-092-3
; Sequence 3, Application US/09984092
; Publication No. US20040037840A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS
; FILE REFERENCE: P1011PC00
; CURRENT APPLICATION NUMBER: US/09/984,092
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
US-09-984-092-3

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 11 Gaps: 1

US-09-493-480-7 (1-712) x US-09-984-092-3 (1-3768)
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Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
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Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGGACATGCTCCGCCACCTCTTACCAGGGCTGCCAGTGTGGAGGAACCTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACTACCTACTGCTCCCGCCCAATGCCAGCTCTTCTTCGAGGATATCCAGGAGGTG 240
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGCTCATCGCTCAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
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Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
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Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCCTCACAGAGATCTTGAAGAGAGGGTCTTGATCCAGCGGAACCCCCAG 480
Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCCTGCTACCAGGACACGATTTTGTGGAGGACATCTTCCACAGAACCAACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCGACCCCTGTTCTCCGATGTGTAAG 600
Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGGATTGTACAGAGCTGACGCGCACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
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Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGGCTGCACGGGCCCAAGCACCTGTGACTGCTGCGCTGCGCTCCACTTCAACCCAC 780
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCACCTGCCCGCCCGTGGTCACTTCAACACACACACAGTTGAG 840
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 901 TACAACTACCTTCTACGAGCGTGGATCTCTGCACCTCGTCTGCCCCCTGCACAAACCAA 960
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1021 GTGTGCTATGCTGGGCATGGAGCACCTTGCAGAGGTGAGGGCAGTTACCAAGTGCCT 1080
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1081 ATCCAGGAGTTTGTGCTGCTGCAAGAAGATCTTTGGAGCGCTGGCATTTCTGCGGAGAGC 1140
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnPhe 400
Db 1141 TTTGATGGGAGCCCGAGCTCCAAACACTGCCCGCTCCAGCCAGAGCAGCTCCCAAGTGT 1200
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 1201 GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGGCGGACAGCTGCCT 1260
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1261 GACCTCAGCGCTCTCCAGAACCTGCAAGTAATCCGGGGAGCAATCTCGCACAATGCGGCC 1320
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1321 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCGCTCACTGAGGGAA 1380
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QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1381 CTGGGAGTGGACTGGCCCTCATCCACCAATAACACCCACCTCTGCTTCGTGCACACGGTG 1440
QY 481 ProTirAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1441 CCTGGGACACAGCTCTTTTGGAAACCCGACCAAGACTCTGCTCCACACTGCGCAACCGGCCA 1500
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1501 GAGGACGAGTGTGGGCGAGGCGCTGGCCCTGCCACAGCTGTGCGCGCGGAGGCACTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1561 TGGGGTCCAGGGGCCCAACCCAGTGTGTCAACTGACGACAGTTCCTTCGGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1621 GTGGAGGAATGCCAGTACTGCGAGGGGCTCCCGAGGAGTATGTGAATGTCAGGCACTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTGCCGTGCCACCTCGAGTGTGAGCCCAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1740
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
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QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
Db 1801 CCAGCGGTGTGAACCTGACCTCTCTACATCCCATCTGGAAGTTTCCAGATGAGGAG 1860
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
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QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGCTGCCCGCCGAGCAGAGAGCGCCCTCTGACGTCCATCGTCTCTGCGGTGGTGGC 1980
QY 653 ----- 653
Db 1981 ATTCTGTGTGTGTGTGGGGGTGGTCTTTGGGATCTCTCAAGCGACGGCAGCAG 2040
QY 653 ----- 653
Db 2041 AAGATCGGAAGTACAGATGCGGAGACTGCTGCGAGAAACGGAGCTGTGTGGAGCCGCTG 2100
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QY 653 ----- 653
Db 2281 CCCAAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGCTGTGTGGGCTCCCCA 2340
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Db 2941 AGGGACCCCGAGCGCTTGTGGTCAATCCAGAAATGAGACTTGGGGCCAGCCAGTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCCTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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QY 705 GlyMetValHisHisArgHisArg 712
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RESULT 8

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US-10-313-644-1
; Sequence 1, Application US/10313644
; Publication No. US20030157119A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: Hand-Zimmerman, Susan
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; FILE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.483C3
; CURRENT APPLICATION NUMBER: US/10/313,644
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-313-644-1
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Alignment Scores: 0 Length: 3768
Pred. No.:

Score:	3776.00	Matches:	712
Percent Similarity:	67.94%	Conservative:	0
Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
DB:	16	Gaps:	1
US-09-493-480-7 (1-712) x US-10-313-644-1 (1-3768)			
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QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
DB	61	GGGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCTCGCCAGTCCCGAG	120
QY	41	ThrHisLeuAspMetLeuAlaHisLeuTyrGlnGlyCysGlnValValGlnGlnGlyAsnLeu	60
DB	121	ACCCACCTGGACATGCTCGGCCACCTCTACCAAGGCTGCAGGTGGTGAGGAAACCTG	180
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
DB	181	GAACTCACCTACTGCGCCCAACCAATGCCAGCTGTCTCTCGAGATATCCAGAGGTG	240
QY	81	GlnGlyTyrValLeuIleAlaHisLeuGlnValArgGlnValProLeuGlnArgLeuArg	100
DB	241	CAGGGCTAGCTCATCGCTCACACCAAGTGAGGCAGTCCCCTGCGAGGGCTGGCG	300
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
DB	301	ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCGCTGTAGACAAATGA	360
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
DB	361	GACCCCCTGAACAATACCACTCTGTCAAGGGCTCTCCCAAGAGGCTCGGGAGCTG	420
QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
DB	421	CAGCTTCGAAGCTCACACAGATCTTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG	480
QY	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla	180
DB	481	CTCTGCTACAGACACGATTTTGTGGAAGGACATCTTCCACAAGAACCAACAGCTGGCT	540
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	541	CTCACACTGATAGACACCAACCGCTCTCGGGCTGCGCACCTCTGTTCTCCGATGTGTAG	600
QY	201	GlySerArgCysTrpGlyGluSerGluAspCysGlnSerLeuThrArgThrValCys	220
DB	601	GGCTCCCGTGTGGGGAGAGATTCTGAGGATTGTGACAGGCTGACGGGCACCTGTCTGT	660
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysHisGlnGlnCys	240
DB	661	GCGGTGGGTGTGCGCGCTGCAAGGGCCACTGCCCACTGACTGTGTCCTGAGCAGTGT	720
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	721	GCTGCCGGCTGACGGGGCCCAAGCACTCTGACTGCTGGCTGGCTGCCCTCCACTTCAACCA	780
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
DB	781	AGTGGCATCTGTGAGCTGACCTGCCAGCCCTGGTCACCTACAAACACACACACACGTTTGA	840
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
DB	841	TCCATGCCCAATCCCGAGGGCCGGTATACATTTGGCGCCAGCTGTGTGACTGCCTGTCCC	900
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	901	TACAACTACTTTCTACGAGCTGGGATCTTGACCCCTGTCTGCCCCCTGCACAAACCAA	960
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
DB	961	GAGGTGACAGAGAGATGGAACACAGCGGTGTGAGAAAGTGACGAAGCCCTGTGCCCCGA	1020
QY	341	ValCysTyrGlyLeuGlyMetClnHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1021	GTGTCTATGTGTCTGGGCATGGAGCATTGGCAGAGGTGAGGGCAGTTACCAAGTGCCAAT	1080
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1081	ATCCAGGAGTTTGTGCTGCTGCAGAGATCTTTGGAGGCTGGCATTTCTGCGGAGAGC	1140
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
DB	1141	TTTGTATGGGACCCAGCTCCAAACAGTCCCGCTCCAGCCAGAGCAGCTCCAAGTGTTT	1200
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
DB	1201	GAGACTCTGGAAGAGATCACAGGTTACCTATATACATCTCAGCATGGCCGACAGCTGCCT	1260
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	1261	GACCTCAGCGTCTTCCAGAACCTGCAGTATATCCGGGACGNAATTCGCACANTGGCGC	1320
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1321	TACTCGCTGACCTGCAAGGGCTGGGCATCAGTGGCTGGGCTGCGCTCACTGAGGAA	1380
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
DB	1381	CTGGGCACTGGACTGGCCCTCATCCACCATAACCCACCTCTGCTTGTGTGCACAGGTG	1440
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	1441	CCCTGGGACCACTCTTTGGNAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1500
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	1501	GAGGACGAGTGTGGCGAGGGCTGGCTGCCACCACTGTGGCCCGCGAGGCACTGC	1560
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	1561	TGGGTCCAGGGGCCCAACCACTGTCACTGACGCCAGTTCCTTCGGGGCCAGGAGTGC	1620
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
DB	1621	GTGGAGGATGCCGAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACGT	1680
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	1681	TTGCGGTGCCACCTGAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGGAG	1740
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
DB	1741	GCTGACCACTGTGTGGCTGTGCCCTATAGGACCTCTCCCTCTGCGTGGCCGCTGC	1800
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
DB	1801	CCCAGGCTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	1860
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLeuLys	640
DB	1861	GGCGCATGCCAGCTTGGCCCATCACTCACTGCCACCCACTCTGTGTGAGACCTGTGATGACA	1920
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
DB	1921	GGCTCCCCCGGAGCAGAGAGCCCTCTGACGTCCATCATCTCTGCGGTGTGTGGC	1980
QY	653	-----	653
DB	1981	ATTCTGCTGCTGCTGCTTGGGGGTGCTTTGGGATCCTCATCAAGCAGCGGAGCAG	2040
QY	653	-----	653

Db 2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2100
QY 653 ----- 653
Db 2101 ACACCTAGCGGAGCGATGCCAACACGAGCGAGATGGGATCCTGAAAGAGACGGAGCTG 2160
QY 653 ----- 653
Db 2161 AGAAGGTGAAGTGTGGATCTGGCGCTTTTGGCAGCTTACAAGGCGATCTGGATC 2220
QY 653 ----- 653
Db 2221 CCTGATGGGAGATGTGAAAATTCAGTGGCCATCAAGTGTGAGGGAAAACACATCC 2280
QY 653 ----- 653
Db 2281 CCCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGTGTGGGTCCCCA 2340
QY 653 ----- 653
Db 2341 TATGTCTCCGCTTCTGGGCATCTGCTGACATCCACGGTGCAGCTGCTGACACAGCTT 2400
QY 653 ----- 653
Db 2401 ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCGCGAGCGCTGGGCTCCAG 2460
QY 653 ----- 653
Db 2461 GACCTGCTGAATGGTGTATGCAGATTGCCAAGGGATGAGCTACCTGGAGGATGTGCGG 2520
QY 653 ----- 653
Db 2521 CTCGTACACAGGACTTGGCGCTCGGAACGTGCTGAGAGTCCCAACCATGTCAAA 2580
QY 653 ----- 653
Db 2581 ATTACAGACTTCGGGCTGGCTCGGCTCTGCGTCTGCGACATTGACAGACAGATACCATGCAGAT 2640
QY 653 ----- 653
Db 2641 GGGGGCAAGTGCCCATCAAGTGTGATGGCGCTGGAGTCCATTCTCCGCGCGGCTTCAAC 2700
QY 653 ----- 653
Db 2701 CACCAGAGTATGTGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
QY 653 ----- 653
Db 2761 AAACCTTACGATGGATCCCGAGCCCGGAGATCCCTGACCTGCTGGAAAAGGGGAGCGG 2820
QY 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTTCAATGTTGGATG 2880
QY 653 ----- 653
Db 2881 ATTGACTCTGAATGTCGCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGAGCCCCCAGCGCTTTGTGTCATCCAGATGAGGACTTGGGCCCGAGCCAGTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGNACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGGTACCCAGCAGGGCTTCTTCTGTCCAGACCTTGCCCCGGCGCTGGG 3120
QY 705 GlyMetValHisArgHisArg 712
Db 3121 GGCATGGTCCACCACAGGCCCGC 3144

RESULT 9

US-10-280-576-3
; Sequence 3, Application US/10280576
; Publication No. US20040044405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280,576
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-280-576-3

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 18 Gaps: 1

US-09-493-480-7 (1-712) x US-10-280-576-3 (1-3768)

QY 1 MetGluLeuAlaAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuProProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTGTGCGCTGGGGCTCTCTCTCGCCCTCTTGCCTCCCGAGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLeuLeuArgLeuProAlaSerProGlu 40
Db 61 GCAGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnValAsnLeu 60
Db 121 ACCACCTGGACATGTCTCCGCACCTCTACACAGGGTGCACAGGTGTGTGCGAGGAAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACTCACCTACCTGCGCCCAATGCAGCTGTCTCTCTGTCAGGATATCCAGGAGGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGCTCATCGCTCAACAAGTGAAGCAGGTCCCACTGTCAGAGGCTGCGG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGCGCCGTGTAGACATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAATAACACCCCTGTCAACAGGGGCTCCCCAGGAGGCTGCGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCCTCAAGAGATCTTGAAGAGGAGGGTCTTGATCCAGCGGAAACCCCGAG 480
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
Db 481 CTCCTGTACAGACACAGATTTTGTGGAAGGACATCTTCCACAAAGAACCAACAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGGCTGCCACCCCTGTTCTCCGATGTGTAAAG 600
QY 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220

Db	601	GGCTCCCGCTGCTGGGAGAGAGATTCTGAGGATTGTGAGAGCTGTGAGCGCACACTGTCTGT	660	QY	581	AlaAspGlnCysValAlaCysAlaHisTyrIysAspProPheCysValAlaArgCys	600
QY	221	AlaGlyGlyCysAlaArgCysIysGlyProLeuProThrAspCysCysHisSgluGlnCys	240	Db	1741	GCTGACCAGTGTGTGGCCTGTGGCCACTATAGGACCCTCCCTTCTGCGTGGCCGCTGC	1800
Db	661	GCGGTGGCTGTGCCCTTGCAAGGGGCCACTGCCCACTGACTGTGCCATGAGCAGTGT	720	Db	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrrPlyPheProAspGluGlu	620
QY	241	AlaAlaGlyCysThrGlyProIysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260	Db	1801	CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	1860
Db	721	GCTGCCGCTGCACGGGCCCAAGCACTCTGACTGCTGGCCTGCCTCCACTTCAACCA	780	QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
QY	261	SerGlyIleCysGlnLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	Db	1861	GGCGATGTCGAGCTGCACTGCCAGGCCCTGGTCACCTACAACACAGACACGTTTGAG	1920
Db	781	AGTGGCATCTGTGAGCTGCACTGCCAGGCCCTGGTCACCTACAACACAGACACGTTTGAG	840	QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300	Db	1921	GGTCCCCCGCGAGACAGAGACGACCTCTGACGTCCATCGTCTCTCGCGGTGGTTGCG	1980
Db	841	TCCATGCCCAATCCGAGGGCCGGTATACATTTCGGGCCAGCTGTGTGACTGCCTGTGTC	900	QY	653	-----	653
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	Db	1981	ATTCTGCTGGTCTGTGGTCTTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	2040
Db	901	TACAACCTACCTTTCTACGGAGCTGGGATCCTTGCACCTCTGTCTGCCCTCGCACAA	960	QY	653	-----	653
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluIysCysSerIysProCysAlaArg	340	Db	2041	AAGATCCGGAAGTACAGATGCGGAGACTGTCTGCGAGGAACCGGAGCTGTGTGGAGCCGCTG	2100
Db	961	GAGGTACACGACGAGGATGGAACACAGCGGTGTGGAAGTGCAGCAAGCCCTGTGCCGA	1020	QY	653	-----	653
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	Db	2101	ACACCTAGCGGAGCGATGCCCAACCGGCGCAGATGCCGATCCTGAAAGACGAGAGCTG	2160
Db	1021	GTGTGCTATGTCTGGGCATGAGACATTCGAGAGGTGAGGCGAGTTACCACTGCCCAAT	1080	QY	653	-----	653
QY	361	IleGlnGluPheAlaGlyCysIysIysIlePheGlySerLeuAlaPheLeuProGluSer	380	Db	2161	AGGAAGTGAAGTGTCTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTG	2220
Db	1081	ATCCAGAGTTTGTGGCTGCAAGAAGATCTTTGGGAGCTGGCATTTCTGCGGAGAGC	1140	QY	653	-----	653
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnValPhe	400	Db	2221	CCTGATGGGGAATGTGAAATTCAGTGGCCATCAAGTGTGAGGAAACACATCC	2280
Db	1141	TTTGATGGGGACCCAGCCCTCAACACTGCCCGCTCCAGCCAGCAGCTCCAAGTGT	1200	QY	653	-----	653
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrrProAspSerLeuPro	420	Db	2281	CCCAAGCCACAAAGAAATCTTAGACGAAGCATACGTGATGGTGGTGGGCTCCCCA	2340
Db	1201	GAGACTCTGGAGAGATACAGGTTACCTATACATCTCAGCATGGCCGACAGCTGCCT	1260	QY	653	-----	653
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	Db	2341	TATGTCTCCGCTTCTGGGCATCTGCCCTGACATCCACGGTGCAGTGTGTGACACAGCTT	2400
Db	1261	GACCTCAGCGTCTTCCAGAACCTGCAAGTAAATCCGGGGACGAATTCGCACAATGGCGC	1320	QY	653	-----	653
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrrPlyLeuArgSerLeuArgGlu	460	Db	2401	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAACCGCGGAGCCTGGGCTCCCAG	2460
Db	1321	TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCACTGAGGGAA	1380	QY	653	-----	653
QY	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480	Db	2461	GACCTGTGAACCTGGTGTATGCAGATTGCCAAGGGGATGAGCTACTCTGGAGGATGTGCGG	2520
Db	1381	CTGGGCACTGGACTGGCCCTCATCCACCAATACACCCACTCTGTCTTGTGACACGGTG	1440	QY	653	-----	653
QY	481	ProTrrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	Db	2521	CTCGTACACAGGGAATTTGGCGCTCGGAACGTGCTGTCAAGAGTCCCAACCATGTCAAA	2580
Db	1441	CCCTGGACACAGCTCTTTCGGAACCGCACCAAGCTCTGCTCCACTGCCAACCGGCCA	1500	QY	653	-----	653
QY	501	GluAspGlyCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	Db	2581	ATTACAGACTTCGGGCTGGCTCGGCTGTGGACATTGACGAGACAGATTACCATGCAGAT	2640
Db	1501	GAGGACGAGTGTGTGGGCGAGGCGCTGGCCTGCCACACAGCTGTGGCGCCGAGGGCACTGC	1560	QY	653	-----	653
QY	521	TrrPlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	Db	2641	GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGCTTCAAC	2700
Db	1561	TGGGTCCAGGGCCCAACCACTGTGTCACTGCAGCCAGTTCCTTCGGGGCCAGANGTC	1620	QY	653	-----	653
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	Db	2701	CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC	2760
Db	1621	GTGGAGAAATCCGAGTACTGACGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACCTGT	1680	QY	653	-----	653
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	Db	2761	AAACCTTAGATGGGATCCAGCCCGGGAGATCCCTGACCTCTGGAAAGGGGAGCGG	2820
Db	1681	TTGGCGTGCCACCTGAGTGTGAGCCCCAGAAATGGCTCAGTCACTGTTTGGACGGAG	1740				

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QY 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGTGTCAAATGTTGGATG 2880
QY 653 ----- 653
Db 2881 ATTGACTCTGAATGTCGGCCCAAGATTCCGGAGTTGGTGTCTGTAATTCTCCCGCATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCCAGCGCTTTGTGGTCATCCAGAAATGAGGACTTGGGCCAGCCAGTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTACCCGAGCAGGGCTTCTTCTGTCCAGACCTGCCCCGGGGCTGGG 3120
QY 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGGTCCACCACAGCCACCGC 3144

RESULT 10
US-10-441-779C-3
; Sequence 3, Application US/10441779C
; Publication No. US20040141958A1
; GENERAL INFORMATION:
; APPLICANT: Steina, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gautam, Anand
; APPLICANT: Haaning, Jesper
; APPLICANT: Dalum, Iben
; APPLICANT: Birk, Peter
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
; FILE REFERENCE: 4614-0116P
; CURRENT APPLICATION NUMBER: US/10/441,779C
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 09/413,186
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/105,011
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: PA 1998 01261
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
; OTHER INFORMATION:
US-10-441-779C-3

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 19 Gaps: 1

US-09-493-480-7 (1-712) x US-10-441-779C-3 (1-3768)

QY 1 MetGluLeuAlaAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20.
Db 1 ATGGAGCTGGCGGCTTGTGCCCGCTGGGGGCTCTCTCTCGCCCTCTTGGCCCGGAGCC 60
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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCAGGACCCCAAGTGTGCACCGGCACAGACATGAAGCTGGGGTCTCCCTGCGCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValGlnGlnGlyAsnLeu 60
Db 121 ACCCACTGGACATGTCTCGGCCACCTCTACCAAGGCTGCCAGGTGGTGGAGGGAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACTCACCTACTGCTGCCACCAATGCGAGCTGTCTCTCTGAGGATATCCAGGAGGTG 240
QY 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGTCTCATCGCTCAACAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGNAACNATACCACTCCCTGTCAAGGGGCTTCCCAAGAGGCTTCCGAGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuLeuGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCTTCACAGAGATCTTGAAGGAGGGTCTTGATCCAGCGGAACCCCGAG 480
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
Db 481 CTCGTCTACAGGACACGATTTTGTGGAAGGACATCTTCACAGAACAAACCAAGCTGGCT 540
QY 181 LeuThrLeuLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCGACCCCTGTTCTCCGATGTGTAG 600
QY 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGCTGGGAGAGAGATTCTGAGGATTGTGAGAGCTGCAGAGCTGCAGCGCACTGTGT 660
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 661 GCGGTGGCTGTGCGCGCTGCAAGGGGCACTGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGGCTGCACGGGCCCCCAAGCACTCTGACTGCTGCGCTGCTGCTGCTGCTGCTGCTG 780
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCCTGCCAGGCTGCTGCACTTACCAACACAGACAGCTTTGAG 840
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 841 TCCATGCCCAATCCCGAGGGCGGTATACATTCGGGCGCCAGCTGTGTGACTGCTGCTGCTGCTG 900
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 901 TACAACTACTTTCTACGGACGTGGGATCTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 961 GAGGTGCACAGCAGAGGATGGACACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGCTGCGCGA 1020
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1021 GTGTGCTATGGTCTGGGCACTTGGAGAGGTGAGGAGGTGAGGAGGTGAGGAGGTGAGGAGGT 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1081 ATCCAGAGTGTGTGGCTGCAAGAGATCTTTGGAGGAGCTTGGCACTTTCTGCGCGGAGAGC 1140
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QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
DB 1141 TTITATGGGGACCCAGCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
DB 1201 GAGACTCTGGAAGAGATCAAGGTTACCTATATACATCTCAGCATGGCGGACAGCCTGCCT 1260
QY 421 AspLeuSerValPheGlnAenLeuGlnValIleArgGlyArgIleLeuHisAenGlyAla 440
DB 1261 GACCTCAGCGTCTTCAGAACCTGCAAGTAATCCGGGGAGCAATCTGCACAAATGGCGCC 1320
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
DB 1321 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGCTGGCTCACTGAGGGAA 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAenThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTCGTGCACACGGTG 1440
QY 481 ProTyrAspGlnLeuPheArgAenProHisGlnAlaLeuLeuHisThrAlaAenArgPro 500
DB 1441 CCTGGGACACAGCTCTTTTCGGAACCCGACACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1500
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACAGTGTGTGGCGGAGGGCTGGCTGCCACAGCTGTGCCCGCGAGGGCACTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAenCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGGTCCAGGGCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1621 GTGGAGGAATCGCGAGTACTGCAGGGGCTCCCGAGGGAGTATGTGAATCCAGGCACCTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAenGlySerValThrCysPheGlyProGlu 580
DB 1681 TTGCCGTGCCACCTGAGTGTGAGCCCCAGAGATGGCTCAGTGACCTGTTTGGACGGAG 1740
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
DB 1741 GCTGACCACTGTGTGGCCTGTGCCCACTATAAGGACCCCTCCCTCTCGCGTGGCCGCTGC 1800
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
DB 1801 CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
QY 621 GlyAlaCysGlnProCysProIleAenCysThrHisSerCysValAspLeuAspLys 640
DB 1861 GGGCATGCCAGCCTTGCCCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAG 1920
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer- 653
DB 1921 GGTGTCGCCCGGAGCAGAGAGCAGCCCTCTGACGTCCATCGTCTCTCGCGTGGTTGGC 1980
QY 653 ----- 653
DB 1981 ATTCTGCTGGTCTGTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGAGCAG 2040
QY 653 ----- 653
DB 2041 AAGATCCGGAAGTACAGATGCGGAGACTGCTGCAGGAACGGAGTGGTGGAGCGCGTG 2100
QY 653 ----- 653
DB 2101 ACACCTAGCGGAGCGATGCCCAACAGCGCGCAGATGCGGATCCTGAAGAGACGGAGCTG 2160
QY 653 ----- 653
DB 2161 AGGAAGTGAAGGTGCTTGATCTGGCGCTTTGGCACAGTCTACAGGGCATCTGGATC 2220
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DB 2221 CCTGATGGGAGAGTGTGAAAATTCCAGTGGCCATCAAAGTCTTGAGGGAAAAACACATCC 2280
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DB 2281 CCAAAGCCAAACAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGCTCCCA 2340
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DB 2341 TATGTCTCCGCGCTTCTGGGCATCTGGGCATCTGCCTGACATCCACGGTGCAGCTGTGTGACACAGCTT 2400
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DB 2401 ATGCCCTATGCTGCTCTTTAGACCATGTTCGGGAAACCCGCGAGCCTGGGCTCCACAG 2460
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DB 2461 GACCTGCTGAACCTGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520
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DB 2521 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGTGTTCAAGAGTCCCACCATGTCAAA 2580
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DB 2581 ATTACAGACTTCGGGCTGGCTCGGCTGTGGACATTGACGAGACAGAGTACCATGCAGAT 2640
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DB 2641 GGGGCAAGGTGCCCATCAAGTGGATGGCGTGGAGTCCATTCTCCGCGCGGTTACCC 2700
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DB 2701 CACCAGAGTATGTGTGGAGTTATGTTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
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DB 2761 AAACCTTAGATGGATCCAGCCCGGAGATCCCTGACCTGCTGMAAAGGGGAGCGG 2820
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DB 2821 CTGCCCCAGCCCCCATCTGCACCATTGTATGTTACATGATCATGTTCAATGTTGGATG 2880
QY 653 ----- 653
DB 2881 ATTGACTCTGATGTGCGGCCAAGATTCCGGGAGTGGTGTCTGAATTCTCCCGCATGGCC 2940
QY 654 -----GlnAenGluAspLeuGlyProAlaSerProLeu 664
DB 2941 AGGGACCCCGCAGCGCTTTGTGTCTATCCAGAATGAGGACTTGGGCCAGCCAGTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684
DB 3001 GACAGACCTTCTACCGCTACTGCTGGAGGACGATGATGCGGACCTGGTGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3061 GAGGAGTATCTGTTACCCAGCAGCAGCGGCTTCTCTGTCCAGACCTTGCCCGGGCGCTGG 3120
QY 705 GlyMetValHisHisArgHisArg 712
DB 3121 GGCATGGTCCACACAGCAGCACCGC 3144
RESULT 11
US-10-384-339C-52
; Sequence 52, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GEN
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; CURRENT FILING DATE: 2003-03-07

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, , PCT/EP02/001552
, , PRIOR APPLICATION NUMBER: 2002-01-09
, , PRIOR FILING DATE: 2002-01-09
, , PRIOR APPLICATION NUMBER: DE 10100586.5
, , PRIOR FILING DATE: 2001-01-09
, , PRIOR APPLICATION NUMBER: DE 10155280.7
, , PRIOR FILING DATE: 2001-10-26
, , PRIOR APPLICATION NUMBER: DE 10158411.3
, , PRIOR FILING DATE: 2001-11-29
, , PRIOR APPLICATION NUMBER: DE 10160151.4
, , PRIOR FILING DATE: 2001-12-07
, , NUMBER OF SEQ ID NOS: 173
, , SOFTWARE: Patentin Ver. 2.1
, , SEQ ID NO 52
, , LENGTH: 3768
, , TYPE: DNA
, , ORGANISM: Homo sapiens
, , PUBLICATION INFORMATION:
, , TITLE: ERBB2
, , PATENT DOCUMENT NUMBER: NMO04448
, , US-10-394-339C-52

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Alignment Scores:					
Pred. No.:	0	Length:	3768		
Score:	3776.00	Matches:	712		
Percent Similarity:	67.94%	Conservative:	0		
Best Local Similarity:	67.94%	Mismatches:	0		
Query Match:	95.50%	Indels:	336		
DB:	19	Gaps:	1		

US-09-493-480-7 (1-712) x US-10-384-339C-52 (1-3768)

Qy	1	MetGluLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGluVal	20
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Qy	21	AlaSerThrGlnValCysThrGlyThrAspMetLeuLeuArgLeuProAlaSerProGlu	40
Db	61	GGCAGCACCCCAAGTGTGCACCGGCACACACATGAAGCTGGGCTCCCTGCCAGTCCGAG	120
Qy	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
Db	121	AGCCACCTGGAGATGCTCGGCACCTCTACACAGGGCTGCCAGGTGGTGCAGGGAACCTG	180
Qy	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
Db	181	GAACCTCACCTACTCGCCACCACCAATGCCAGCTGTCTCTCTGAGGATATCCAGGAGGTG	240
Qy	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	241	CAGGGCTACGTGCTCATCGCTCACAAACAAAGTGAAGCAGGTGCCACCTCCAGAGGCTCGCG	300
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
Db	301	ATTGTGCGAGGCCACCCAGCTCTTTGAGGACAACTATGCCCCTGGCCGTCTAGACAATGGA	360
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	361	GACCCGCTGAACAATACCAACCCCTGTCAAGGGGCTCCCCAGAGGCGCTCGCGGAGCTG	420
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
Db	421	CAGCTTCGAAGGCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCCCAG	480
Qy	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
Db	481	CTCTGCTACCGAGACACGATTTTGTGGAAGGACATCTTCCACAAGAAACAACAGCTGGCT	540
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	541	CTCACACTGATAGACCAACCGCTCTCGGGCCCTGCCACCCCTGTCTCCGATGTGTAG	600
Qy	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220

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QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 1741 GTGACCATGTGTGGCCCTGTGCCCACTATAGGACCCCTCCCTTCGTGGTGCCCGCTGC 1800

QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1801 CCCAGGGTGTGAACCTGACCTCTCTACATGTCCTCATCTGGAAGTTTCCAGATGAGGAG 1860

QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db 1861 GCGCATGCGACGCTTGCCCCATCAACTGCACCCACTCCTGTGTGACCTGGATGACAA 1920

QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGCTGCCCCCGCAGCAGAGAGCCGCTCTGACGTCCATCGTCTCTCGGTGGTTGGC 1980

QY 653 ----- 653
Db 1981 ATTCTGCTGGTGTCTTTGGGGTGGTCTTTGGGATCCTCATCAAGCGCGGAGCG 2040

QY 653 ----- 653
Db 2041 AAGATCCGGAAGTACAGATGCGGAGTGTCTCAGGAAACGAGCTGTGGAGCGGCTG 2100

QY 653 ----- 653
Db 2101 ACACCTAGCGGAGCGATGCCAACCGAGCGCAGATGCGGATCCTGNAAGAGAGGCTG 2160

QY 653 ----- 653
Db 2161 AGGAAGGTGAAGTGTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220

QY 653 ----- 653
Db 2221 COTGATGGGGAATGTGAAATTCAGTGGCCATCAAAAGTTGTGAGGAAACACATCC 2280

QY 653 ----- 653
Db 2281 CCCAAGCCAAACAGAAATCTTAGCAGCATAGTGTGGTGGTGGTGGCTCCCA 2340

QY 653 ----- 653
Db 2341 TATGTCTCCGCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGTGTGACAGCTT 2400

QY 653 ----- 653
Db 2401 ATGCCCTATGGTGCCTTTAGACCATGTCCGGAAACCGCGAGCGCTGGGCTCCAG 2460

QY 653 ----- 653
Db 2461 GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGATGAGCTACCTGGAGATGTGCG 2520

QY 653 ----- 653
Db 2521 CTGATACAGGAGTGTGGCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAA 2580

QY 653 ----- 653
Db 2581 ATTACAGACTTCGGGCTGGCTCGGCTGTGGACATTGACGACAGAGTACCATGCAGAT 2640

QY 653 ----- 653
Db 2641 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTCCAC 2700

QY 653 ----- 653
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QY 653 ----- 653
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QY 653 ----- 653
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QY 653 ----- 653
Db 2881 ATTGACTCTGAATGTGCGCCAAGATTCCGGGAGTTGGTGTCTGAAATTTCTCCGCATGGCC 2940

QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGACGGCTTTGGTGTATCCAGATAGGACTTTGGGCCCGACCCAGTCCCTTG 3000

QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACTTCTACCGTCTACTGTGGAGGACGATGACATGGGGACCTGTGGATGCT 3060

QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGGTACCAGCAGCGGCTTCTTCTCCAGACCTGCCCGCGCGCTGGG 3120

RESULT 12
US-09-441-411-5
; Sequence 5, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 10 Gaps: 1

US-09-493-480-7 (1-712) x US-09-441-411-5 (1-4473)

QY 1 MetGluLeuAlaAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 175 ATGGAGCTGGCGCCCTTGTGCGCTGGGGCTCTCTCTCGCCCTCTTGGCCCCCGGAGCC 234

QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCGAGCACCAAGTGTGCACCGGCACACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG 294

QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCACCTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGGTGTGTCAGGAAACCTG 354

QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACTCACTACCTGCCCCCAACCAATGCCAGCTGTCTTCTCTCAGAGATATCCAGGAGTG 414

QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
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Db 415 CAGGGCTACGTGCTCATCGCTCACACCAAGTAGGAGCGGTGCCACTGCAGAGCTCGG 474
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 475 ATTGTGCGAGCACCCAGCTCTTTGAGGACAACATATATGCCCTGGCCGTGTAGACAAATGGA 534
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 535 GACCCCGTGAACAATAACACCCCTGTTCACAGGGGCTCTCCACAGAGGCTCGCGGAGCTG 594
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 595 CAGCTTGAAGCTTCACAGAGATCTTGAAGAGAGGGTCTTTGATCCAGCGCAACCCCCAG 654
Qy 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 655 CTCTGCTACCGAGACAGATTTTGTGAAGAGACATCTTCCACAAGAACACAGCTGGCT 714
Qy 181 LeuThrIleuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 715 CTCACACTGATAGACACCAACCGCTCTCGGGGCTTGCACACCCCTGTTCTCCGATGTGTAG 774
Qy 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 835 GCCGGTGGCTGTGCCGCTCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 894
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 895 GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGCTGCGCTGCGCTCCACTTCAACCAC 954
Qy 261 SerGlyIleCysGlnLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 955 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTTACACACAGACAGCTTTGAG 1014
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 1015 TCCATGCCCAATCCCGAGGCGCGGTATACATTCGGGCCAGCTGTGTGACTGCTGTCCC 1074
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1075 TACAACCTACCTTTCTACGAGCTGGGATCTCGACCCCTGCTGCGCCCTGCACAACCAA 1134
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 1135 GAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA 1194
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1195 GTGTGATATGCTTGGGCATGGAGCACTTGGGAGAGGTGAGGCGAGTTACCACTGCCAAT 1254
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1255 ATCCAGAGTTTCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCAATTTCTCGCGGAGAGC 1314
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGlnLeuGlnValPhe 400
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Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
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Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
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Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
Db 1495 TACTCGCTGACCCCTGCAAGGGCTGGGCACTCAGCTGGCTGGGGCTCACTGAGGGAA 1554

Qy 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
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Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1735 TGGGTCCAGGGGCCACCCAGTGTCTCACTGCAGCCAGTTCTTCTGGGGCCAGGAGTGC 1794
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Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
Db 1915 GCTGACCACTGTGTGGCTGTGCCACTATAAGGACCTCCCTTCTGCGTGGCCGCTGC 1974
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1975 CCAGCGGTGTGAAACCTGACCTCTCTATATGCCATCTGGAAGTTTCCAGATGAGGAG 2034
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 2035 GGGCATGTGACGCTTGGCCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAG 2094
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 2095 GGCTGCCCGCGAGCAGAGAGCCGCTCTGACCTCCATCATCTCTGCGGTGGTTGGC 2154
Qy 653 ----- 653
Db 2155 ATTTCTGCTGCTGCTGCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGAGCAG 2214
Qy 653 ----- 653
Db 2215 AAGATCCGGAAGTACAGATGGGAGACTGTGTCAGGAAACGGAGCTGGTGGAGCCGCTG 2274
Qy 653 ----- 653
Db 2275 ACACCTAGCGGAGCGATGCCAACAGGCGCAGATCGGATCCTGAAAGAGAGCGGAGCTG 2334
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Db 2335 AGGAAGGTGAAGTGTCTGGATCTGGCGCTTTTGGCACAGTCTTCAAGGGCATCTGGATC 2394
Qy 653 ----- 653
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Qy 653 ----- 653
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Qy 653 ----- 653
Db 2575 ATGCCCTATGGCTGCTCTTTAGACCATGTCTCGGGGAAACCGCGGACGCTTGGGCTGCCAG 2634

QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluYysCysSerLysProCysAlaArg	340	QY	653	-----	653
DB	1135	GAGGTGACAGCAGAGGATGAAACACACACGGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA	1194	DB	2215	AAGATCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG	2274
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	QY	653	-----	653
DB	1195	GTGTGCTATGCTTGGGATGGAGCACTTGCAGAGGTGAGGCGAGTTTACAGTGGCAAT	1254	DB	2275	ACACCTAGCGAGCGATGTCACCAACAGGCGCAGATGCGGATCTCTGAAAGAGACGGAGCTG	2334
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	QY	653	-----	653
DB	1255	ATCCAGAGTTTGTGCTGTCAGAGAGATCTTTGGGAGCTTGGCATTTCTGCCGAGAGC	1314	DB	2335	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGCTTACAAAGGGCATCTGGATC	2394
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400	QY	653	-----	653
DB	1315	TTTGATGGGACCCAGCCTCCAACTGCCCGCTCCAGCCAGCAGAGCAGCTCCAAGTGT	1374	DB	2395	CTGTATGGGAGAATGTGAAATTCAGATGCGCATCAAAAGTGTGTAGGAGGAAAAACATCC	2454
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	QY	653	-----	653
DB	1375	GAGACTCTGGAAGAGATCAAGGTACCTATATACATCTCAGCATGGCCGAGCAGCTGCCT	1434	DB	2455	CCAAAGCCAAAGAAATCTTTAGACGAAGCATACGTGATGGCTGTGTGGGCTCCCCA	2514
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyVala	440	QY	653	-----	653
DB	1435	GACCTCAGCGTCTTCAGAACCTTGCAAGTAATCCGGGAGCAATCTGCACATATGGGCC	1494	DB	2515	TATGTCTCCCGCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT	2574
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460	QY	653	-----	653
DB	1495	TACTCGTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGCTGGCTCACTGAGGGAA	1554	DB	2575	ATGCCCTATGGCTGCCTTTAGACCATGTCCGGGAAAAACCGCGGACGCTGGGCTCCAG	2634
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480	QY	653	-----	653
DB	1555	CTGGGAGTGGACTGGGCCCTCATCCACATAACACCCACCTCTGCTTCGTGCACACGCTG	1614	DB	2635	GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGATGAGTACCTGGAGGATGTGCGG	2694
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	QY	653	-----	653
DB	1615	CCCTGGACAGCTCTTTCGAAACCCGACCAAGCTCTGCTCCACTGCTCCAAACCGGCCA	1674	DB	2695	CTCGTACACAGGAGCTTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAA	2754
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	QY	653	-----	653
DB	1675	GAGGACAGTGTGTGGCGAGGGCTTGGCTGCCACAGCTGTGGCGCCGAGGCGACTGC	1734	DB	2755	ATTACAGACTTCGGGCTGGCTCGGCTGCTGACATTGACGAGACAGAGTACCATGCAGAT	2814
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	QY	653	-----	653
DB	1735	TGGGTGTCAGGGGCCACCCAGTGTGTCACTGCAGCCAGTTCTCTCGGGGCCAGGATGC	1794	DB	2815	GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTTCTCGCGCGCGGTTCAAC	2874
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAlaAlaArgHisCys	560	QY	653	-----	653
DB	1795	GTGAGGAAATGCCAGTACTGCAAGGGCTCCCAAGGAGTATGTGAATGCCAGGCACTGT	1854	DB	2875	CACCAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGAGGTGATGACTTTTGGGGCC	2934
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	QY	653	-----	653
DB	1855	TTGCCGTGCCACCTGAGTGTACGCCCCAGAAATGGCTCAGTGACCTGTGTTTGGACCGAG	1914	DB	2935	AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGCTGGAAAAAGGGGAGCGG	2994
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600	QY	653	-----	653
DB	1915	GCTGACCAAGTGTGGGCTGTGCCCACTATAAGGACCTCCCTTCTGCGTGGCGCGCTGC	1974	DB	2995	CTGCCCAAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAATGTTGATG	3054
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620	QY	653	-----	653
DB	1975	CCAGCGGTGTAAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATAGGAG	2034	DB	3055	ATTGACTCTGAATGTCCGCCAAGATTCCGGGAGTTGGTGTCTGNAATTTCTCCCGCATGGCC	3114
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640	QY	654	-----	654
DB	2035	GGCGCATGCCAGCTTGCCCCCATCACTGACCCCACTCTCTGTGTGGACCTGGATGACAAG	2094	DB	3115	AGGAGCCCCCAGCGCTTTGGTGTATCCAGAAATGAGGACTTGGGCCAGCAGCTCCCTTG	3174
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653	QY	665	AppSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684
DB	2095	GGCTGCCCCCGAGCAGAGAGCAGCGCTCTGACGTCCATCATCTCTGCGGTGGTTGGC	2154	DB	3175	GACAGACCTTCTACCGCTCCTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT	3234
QY	653	-----	653	QY	685	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly	704
DB	2155	ATTCTGCTGTGTGCTTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	2214	DB	3235	GAGAGTATCTGTGTACCCAGCAGGGCTTCTTCTGTCCAGACCTTGCCTCCCGGGCGCTGGG	3294
QY	705	GlyMetValHisHisArgHisArg	712	QY	705	GlyMetValHisHisArgHisArg	712

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Db      3295 GGCAATGGTCCACACAGGACCGC 3318
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RESULT 14
US-10-207-655-44
; Sequence 44, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; NUMBER OF SEQ ID NOS: 25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-44

Alignment Scores:
Pred. No.:      0      Length:      4473
Score:          3776.00    Matches:      712
Percent Similarity: 67.94%    Conservative: 0
Best Local Similarity: 67.94%    Mismatches: 0
Query Match:      95.50%    Indels:      336
DB:              15      Gaps:      1

US-09-493-480-7 (1-712) x US-10-207-655-44 (1-4473)
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QY      21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db      235 GCGAGACCCCAAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCCTGCCAGTCCCGAG 294
QY      41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db      295 ACCCACTGGACATGTCCGCCACCTCTACCAAGGCTGCCAGGTGTGTCAGGGAACCTG 354
QY      61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db      355 GAACCTACACTCTGCCCAACCAATGCCAGCTGTCTCTTCTGCAGATATCCAGAGGTG 414
QY      81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db      415 CAGGGCTAGTCTCATCGCTCAACCAAGTAGGCGAGTCCCACTGCAGAGGCTGCGG 474
QY      101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db      475 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGACAATGGA 534
QY      121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyCysLeuArgGluLeu 140
Db      535 GACCCGCTGAACAATACCACTGTGCAGGGGCTCCCAAGAGGCTGCGGGAGCTG 594
QY      141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db      595 CAGCTTCGAAGCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCCCAG 654
QY      161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db      655 CTCCTGCTACGAGCACACGATTTTGTGAAGGACATCTTCCACAAGAAACAACAGCTGGCT 714
QY      181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db      715 CTCACACTGATAGACCAACCGCTCTCGGGCTGCCACCTGTCTCTCCGATGTGAAG 774
QY      201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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QY      241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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QY      261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db      955 AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGTGTCACCAACACACAGACAGCTTTGAG 1014
QY      281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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QY      301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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QY      321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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QY      341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
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QY      361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db      1255 ATCCAGGAGTTTGTGCTGCTGCAAGAGATCTTTGGAGCTGGCATTTCTGCGGAGAGC 1314
QY      381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db      1315 TTTGATGGGACCCAGCCTCAACACCTGCCCGCTCCAGCCAGCAGCAGCTCCAAGTGTGT 1374
QY      401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db      1375 GAGACTCTGGAGAGATCACAGGTTCCTATATACATCTCAGCATGCGCGGACAGCTGCTGCT 1434
QY      421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
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QY      461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
Db      1555 CTGGCAGTGGACTGGCCCTCATCCACCATAAACCCACCTCTGCTTCTGTCACACGGTG 1614
QY      481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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QY      501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db      1675 GAGGACGAGTGTGTGGCGAGGGCTGGCCCTGCCACCACTGCTGCGCCGCGGACACTGC 1734
QY      521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db      1735 TGGGTCCAGGGCCCAACCCAGTGTGTCACTGCACAGTTCCTCTCGGGGCGCAGAGTGC 1794
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Db 1915 GCTGACCAAGTGTGGGCTGTGCCCACTATAAGACCCCTCCCTTCGTGCGTGGCCGCTGC 1974
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
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Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
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US-10-101-510-81
; Sequence 81, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WANG, JACKSON
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR FILING DATE: 60/276,947
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
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Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 15 Gaps: 1
US-09-493-480-7 (1-712) x US-10-101-510-81 (1-4473)
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Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCAGCACCACCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGTCAGTCCGAG 294
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
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Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACCTACCTACTGCGCCACCAATGCGAGCTGCTCTCTCTGAGGATATCCAGGAGTG 414
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100

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Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuLeuIleGlnArgAsnProGln	160
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Qy	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
Db	655	CTCTGTACAGGACACGATTTTGTGGAGGACATCTTCCAAAGAACACACCACTGGCT	714
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Db	835	GCGGTGGTGTGCCCGCTGCAAGGGGCCACTGCCCACTGACTGTCGCATGACAGCTGT	894
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Db	1315	TTTGTATGGGACCCAGCCTCCAACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1374
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Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyVala	440
Db	1435	GACCTCAGGCTTTTCCAGNACCTGCAGTAATCCGGGAGCGAATTTCTGCATATGGCGCC	1494
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